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STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-14

Query Match 96.8%; Score 692; DB 1; Length 137;
Best Local Similarity 97.1%; Pred. No. 8.4e-76;
Matches 132; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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DB 2 SSSFDKGRYKGGDASYEPTGPTLVNVTGVDSKGNELLSPHYVEPIKPGTTLTKRKI 61
QY 61 EYVEWALDAPYKKEFRVVELDPSAKIEVYTYDKNKKKEETKSPPIIEKGAVVDLSEHI 120
DB 62 EYVEWALDAPYKKEFRVVELDPSAKIEVYTYDKNKKKEETKSPPIIEKGAVVDLSEHI 121
QY 121 KNPGFNLTIKVIEKK 136
DB 122 KNPGFNLTIKVIEKK 137

RESULT 13
US-08-852-299-14
Sequence 14, Application US/08852299
Patent No. 6010897
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schlott, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,299
FILING DATE: 17-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,261
FILING DATE:
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-299-14

Query Match 96.8%; Score 692; DB 3; Length 137;
Best Local Similarity 97.1%; Pred. No. 8.4e-76;
Matches 132; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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DB 2 SSSFDKGRYKGGDASYEPTGPTLVNVTGVDSKGNELLSPHYVEPIKPGTTLTKRKI 61
QY 61 EYVEWALDAPYKKEFRVVELDPSAKIEVYTYDKNKKKEETKSPPIIEKGAVVDLSEHI 120
DB 62 EYVEWALDAPYKKEFRVVELDPSAKIEVYTYDKNKKKEETKSPPIIEKGAVVDLSEHI 121
QY 121 KNPGFNLTIKVIEKK 136
DB 122 KNPGFNLTIKVIEKK 137

RESULT 14
US-08-256-261-12
Sequence 12, Application US/08256261
Patent No. 5801037
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schlott, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-12

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Best Local Similarity 97.1%; Pred. No. 1.9e-75;
Matches 132; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB 2 SSSFDKGRYKGGDASYEPTGPTLVNVTGVDSKGNELLSPHYVEPIKPGTTLTKRKI 61
QY 61 EYVEWALDAPYKKEFRVVELDPSAKIEVYTYDKNKKKEETKSPPIIEKGAVVDLSEHI 120

Db 62 EYVEWALDATAKEFRVVELDPSAKIEVTYDKNKKKEETKSPITEKGFVVPDLSEHI 121
 QY 121 KNPGENLITKVVIEKK 136
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 Db 122 KNPGENLITKVVIEKK 137

RESULT 15
 US-08-852-299-12
 ; Sequence 12, Application US/08852299
 ; Patent No. 6010897
 ; GENERAL INFORMATION:
 ; APPLICANT: Behnke, Detlef
 ; APPLICANT: Schlott, Bernhard
 ; APPLICANT: Albrecht, Sybille
 ; APPLICANT: G hrs, Karl-Heinz
 ; APPLICANT: Hartmann, Manfred
 ; TITLE OF INVENTION: Expression of signal-peptide-free
 ; TITLE OF INVENTION: staphylokinases
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852,299
 ; FILING DATE: 17-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/256,261
 ; FILING DATE:
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 137 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-852-299-12

Query Match 96.4%; Score 689; DB 3; Length 137;
 Best Local Similarity 97.1%; Pred. No. 1.9e-75;
 Matches 132; Conservative 0; Mismatches 4; Indels 0; Gaps
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 Db 2 SSSFDKGYKKGDDASYFEPTGPLYMVNVTGVDKSGNELLSPHYVEFPKPGTTLTKKI 61
 |||||
 QY 61 EYVEWALDATAKEFRVVELDPSAKIEVTYDKNKKKEETKSPITEKGFVVPDLSEHI 120
 |||||
 Db 62 EYVEWALDATAKEFRVVELDPSAKIEVTYDKNKKKEETKSPITEKGFVVPDLSEHI 121
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 QY 121 KNPGENLITKVVIEKK 136
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 Db 122 KNPGENLITKVVIEKK 137

Search completed: April 22, 2002, 10:41:49
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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:41:55 ; Search time 23.85 Seconds
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422.389 Million cell updates/sec

Title: US-09-601-490-1

Perfect score: 136
Sequence: 1 SSSFDKGYKKKGDDASYEP.....SEHIKNPGENLTKVIEKK 136

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Gapex 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size: 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	136	100.0	136	14	AAW03102
7	136	100.0	136	17	AAW03085
8	136	100.0	136	17	AAW03085
9	136	100.0	136	20	AAW03085
10	136	100.0	136	20	AAW03085
11	136	100.0	136	20	AAW03085

12	131	96.3	136	20	AAW03086	Staphylokinase var
13	130	95.6	136	17	AAW03087	Staphylokinase der
14	129	94.9	136	17	AAW03101	Staphylokinase der
15	129	94.9	136	20	AAW03086	Staphylokinase var
16	129	94.9	136	20	AAW03086	Staphylokinase var
17	129	94.9	136	20	AAW03086	Staphylokinase var
18	126	92.6	136	17	AAW03076	Staphylokinase der
19	126	92.6	136	17	AAW03088	Staphylokinase der
20	118	86.8	136	17	AAW03100	Staphylokinase der
21	118	86.8	136	17	AAW03084	Staphylokinase der
22	114	83.8	136	17	AAW03083	Staphylokinase der
23	114	83.8	136	17	AAW03099	Staphylokinase der
24	107	78.7	136	17	AAW03082	Staphylokinase der
25	107	78.7	136	17	AAW03098	Staphylokinase der
26	102	75.0	136	13	AAW03098	Staphylokinase der
27	102	75.0	136	19	AAW03098	Staphylokinase der
28	102	75.0	136	19	AAW03098	Staphylokinase der
29	102	75.0	136	19	AAW03098	Staphylokinase der
30	102	75.0	136	19	AAW03098	Staphylokinase der
31	102	75.0	136	19	AAW03098	Staphylokinase der
32	102	75.0	136	19	AAW03098	Staphylokinase der
33	102	75.0	136	19	AAW03098	Staphylokinase der
34	101	74.3	136	17	AAW03077	Staphylokinase der
35	101	74.3	136	17	AAW03089	Staphylokinase der
36	101	74.3	136	20	AAW03021	Staphylokinase var
37	101	74.3	136	20	AAW03021	Staphylokinase var
38	100	73.5	136	21	AAW03021	Staphylokinase var
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44	95	69.9	136	17	AAW03097	Staphylokinase der
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47	93	68.4	136	14	AAW03047	Staphylokinase var
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61	91	66.2	136	20	AAW03080	Staphylokinase der
62	90	65.4	136	19	AAW03080	Staphylokinase der
63	89	65.4	136	20	AAW03080	Staphylokinase der
64	85	62.5	136	17	AAW03095	Staphylokinase der
65	85	62.5	136	17	AAW03095	Staphylokinase der
66	81	59.6	136	20	AAW03095	Staphylokinase der
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77	74	54.4	136	19	AAW03074	Staphylokinase der
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84	73	53.7	136	20	AAW03066	Staphylokinase var

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86	73	53.7	136	20	AAV15042	Staphylokinase var	159	15	11.0	15	22	AAE61910	S. aureus staphylo
87	73	53.7	136	20	AAV15037	Staphylokinase var	160	15	11.0	15	22	AAE99435	Staphylokinase min
88	73	53.7	136	20	AAV15022	Staphylokinase var	161	15	11.0	15	22	AAE99435	Staphylokinase min
89	73	53.7	136	20	AAV15032	Staphylokinase var	162	14	10.3	17	7	AAE61715	Fragment of sak ge
90	73	53.7	136	20	AAV15059	Staphylokinase var	163	13	9.6	17	22	AAE99423	Staphylokinase min
91	73	53.7	136	20	AAV15041	Staphylokinase var	164	13	9.6	17	22	AAE99434	Staphylokinase min
92	73	53.7	136	20	AAV15030	Staphylokinase var	165	12	8.8	12	15	AAE67028	Staphylokinase min
93	73	53.7	136	20	AAV15053	Staphylokinase var	166	12	8.8	12	15	AAE67028	Staphylokinase min
94	73	53.7	136	20	AAV15002	Staphylokinase var	167	12	8.8	12	15	AAE67030	Fibrinolytic pepti
95	71	52.2	136	17	AAW03078	Staphylokinase var	168	12	8.8	12	15	AAE67030	Fibrinolytic pepti
96	71	52.2	136	17	AAW03078	Staphylokinase var	169	12	8.8	12	15	AAE67030	Fibrinolytic pepti
97	71	52.2	136	17	AAW03092	Staphylokinase der	170	12	8.8	12	15	AAE67030	Fibrinolytic pepti
98	67	49.3	136	19	AAW44694	Staphylokinase var	171	12	8.1	11	22	AAE99413	Staphylokinase min
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103	64	47.1	136	20	AAV15069	Staphylokinase var	176	11	8.1	11	22	AAE99415	Staphylokinase T-C
104	64	47.1	136	20	AAV15056	Staphylokinase var	177	11	8.1	11	22	AAE99416	Staphylokinase T-C
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108	64	47.1	136	20	AAV15045	Staphylokinase var	181	11	8.1	11	22	AAE99420	Staphylokinase T-C
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135	55	40.4	136	20	AAV15032	Staphylokinase var	208	7	5.1	17	22	AAE99406	Staphylokinase min
136	55	40.4	136	20	AAV15032	Staphylokinase var	209	7	5.1	17	22	AAE99406	Staphylokinase min
137	51	37.5	136	19	AAW44691	Staphylokinase var	210	7	5.1	17	22	AAE99406	Staphylokinase min
138	48	35.3	109	7	AAE60796	Fragment of sak ge	211	7	5.1	17	22	AAE99406	Staphylokinase min
139	47	34.6	136	20	AAV15065	SakSTAR (K35A, E65	212	7	5.1	17	22	AAE99406	Staphylokinase min
140	47	34.6	136	20	AAV15070	Staphylokinase var	213	7	5.1	17	22	AAE99406	Staphylokinase min
141	47	34.6	136	20	AAV15071	SakSTAR (K35A, E65	214	7	5.1	17	22	AAE99406	Staphylokinase min
142	47	34.6	136	20	AAV15055	Staphylokinase var	215	7	5.1	17	22	AAE99406	Staphylokinase min
143	34	25.0	136	20	AAV15072	Staphylokinase var	216	7	5.1	17	22	AAE99406	Staphylokinase min
144	34	25.0	136	20	AAV15072	Staphylokinase var	217	7	5.1	17	22	AAE99406	Staphylokinase min
145	33	24.3	158	12	AAE12138	Staphylokinase gen	218	7	5.1	17	22	AAE99406	Staphylokinase min
146	31	22.8	136	20	AAV15073	Staphylokinase-50m	219	7	5.1	17	22	AAE99406	Staphylokinase min
147	31	22.8	136	20	AAV15074	Staphylokinase var	220	7	5.1	17	22	AAE99406	Staphylokinase min
148	31	22.8	136	20	AAV15075	Staphylokinase var	221	7	5.1	17	22	AAE99406	Staphylokinase min
149	28	20.6	135	21	AAE01298	Altered staphyloki	222	7	5.1	17	22	AAE99406	Staphylokinase min
150	17	12.5	17	22	AAE99400	Staphylokinase var	223	7	5.1	17	22	AAE99406	Staphylokinase min
151	17	12.5	17	22	AAE99401	Staphylokinase var	224	7	5.1	17	22	AAE99406	Staphylokinase min
152	17	12.5	17	22	AAE99402	Staphylokinase var	225	7	5.1	17	22	AAE99406	Staphylokinase min
153	17	12.5	17	22	AAE99403	Staphylokinase var	226	7	5.1	17	22	AAE99406	Staphylokinase min
154	17	12.5	17	22	AAE99404	Staphylokinase var	227	7	5.1	17	22	AAE99406	Staphylokinase min
155	17	12.5	17	22	AAE99405	Staphylokinase var	228	7	5.1	17	22	AAE99406	Staphylokinase min
156	16	11.8	17	22	AAE99422	Staphylokinase var	229	6	4.4	8	18	AAE99406	Staphylokinase min
157	16	11.8	17	22	AAE99436	Staphylokinase min	230	6	4.4	8	18	AAE99406	Staphylokinase min

231	6	4.4	9	21	AAV86687	Telomerase peptide	304	6	4.4	231	22	AAV868902	Neisseria meningit
232	6	4.4	9	21	AAV86713	Telomerase peptide	305	6	4.4	231	22	AAV868903	Neisseria meningit
233	6	4.4	9	21	AAV86819	Telomerase peptide	306	6	4.4	231	22	AAV868904	Neisseria meningit
234	6	4.4	10	21	AAV96394	HLA-A2 binding pep	307	6	4.4	231	22	AAV868905	Neisseria meningit
235	6	4.4	13	18	AAV66936	Peptide epitope 29	308	6	4.4	231	22	AAV868906	Neisseria meningit
236	6	4.4	14	18	AAV66936	Peptide epitope 31	309	6	4.4	231	22	AAV868907	Neisseria meningit
237	6	4.4	17	18	AAV66936	Peptide epitope 8	310	6	4.4	231	22	AAV868908	Neisseria meningit
238	6	4.4	17	18	AAV66936	Peptide epitope 31	311	6	4.4	231	22	AAV868909	Neisseria meningit
239	6	4.4	18	18	AAV66917	Peptide epitope 9	312	6	4.4	231	22	AAV868910	Neisseria meningit
240	6	4.4	18	18	AAV66917	Peptide epitope 12	313	6	4.4	231	22	AAV868911	Neisseria meningit
241	6	4.4	19	18	AAV66915	Peptide epitope 10	314	6	4.4	231	22	AAV868912	Neisseria meningit
242	6	4.4	19	18	AAV66918	Peptide epitope 13	315	6	4.4	231	22	AAV868913	Neisseria meningit
243	6	4.4	19	21	AAV95831	Native mouse 19G1	316	6	4.4	231	22	AAV868914	Neisseria meningit
244	6	4.4	31	21	AAV60877	Arabisdopsis thalia	317	6	4.4	235	18	AAV26692	Toxoplasma gondii
245	6	4.4	32	21	AAV658091	Arabisdopsis thalia	318	6	4.4	235	21	AAV616943	Toxoplasma gondii
246	6	4.4	36	21	AAV42295	CD47 extracellular	319	6	4.4	236	21	AAV57749	Toxoplasma gondii
247	6	4.4	41	18	AAV66905	CD47 extracellular	320	6	4.4	241	22	AAV86648	S. pneumoniae muta
248	6	4.4	51	22	AAV64883	Human secreted pro	321	6	4.4	244	21	AAV65866	Arabisdopsis thalia
249	6	4.4	62	21	AAV646286	Arabisdopsis thalia	322	6	4.4	247	21	AAV652296	Arabisdopsis thalia
250	6	4.4	63	22	AAV18293	Peptide #4727 enco	323	6	4.4	250	21	AAV63222	Arabisdopsis thalia
251	6	4.4	73	21	AAV60884	Human secreted pro	324	6	4.4	259	22	AAV64664	Hydroxyindol-relat
252	6	4.4	77	21	AAV60886	Human secreted pro	325	6	4.4	259	22	AAV62248	Rat insulin-respon
253	6	4.4	92	21	AAV602036	Human secreted pro	326	6	4.4	263	21	AAV65865	Arabisdopsis thalia
254	6	4.4	99	22	AAV69310	Human secreted pro	327	6	4.4	266	21	AAV41386	Human ORF ORF1150
255	6	4.4	104	21	AAV833028	Pinus radiata tran	328	6	4.4	272	18	AAV26698	Toxoplasma gondii
256	6	4.4	106	19	AAV86028	S. pneumoniae derl	329	6	4.4	272	21	AAV54420	Secoisolariciresin
257	6	4.4	135	21	AAV627690	Arabisdopsis thalia	330	6	4.4	273	21	AAV54412	Secoisolariciresin
258	6	4.4	135	21	AAV67151	Arabisdopsis thalia	331	6	4.4	276	21	AAV54416	Secoisolariciresin
259	6	4.4	139	19	AAV66427	Amino end of the	332	6	4.4	277	18	AAV55605	H. pylori ORF 14ce
260	6	4.4	141	20	AAV35818	Amino acid sequenc	333	6	4.4	277	21	AAV54413	Secoisolariciresin
261	6	4.4	141	21	AAV27689	Arabisdopsis thalia	334	6	4.4	277	21	AAV54415	Secoisolariciresin
262	6	4.4	141	21	AAV67150	Arabisdopsis thalia	335	6	4.4	278	16	AAV72597	Ostertagia proteic
263	6	4.4	142	18	AAV66904	CD47 extracellular	336	6	4.4	287	22	AAV65782	Cysteine protease
264	6	4.4	146	21	AAV601541	Human secreted pro	337	6	4.4	288	21	AAV636221	Arabisdopsis thalia
265	6	4.4	149	21	AAV52502	Helicobacter pylor	338	6	4.4	293	18	AAV55218	H. pylori ORF 02ce
266	6	4.4	150	21	AAV83821	Plasmid pCHO-shlAP	339	6	4.4	294	22	AAV83176	Coriobacterium th
267	6	4.4	153	19	AAV68799	H. pylori GHPO 128	340	6	4.4	307	22	AAV81714	S. epidermidis ope
268	6	4.4	155	22	AAV75168	Human colon cancer	341	6	4.4	319	19	AAV72059	HSV-2 strain SB5 C
269	6	4.4	158	21	AAV52493	Helicobacter pylor	342	6	4.4	320	14	AAV33279	43 kd endotlagel
270	6	4.4	164	21	AAV27688	Arabisdopsis thalia	343	6	4.4	320	21	AAV62855	Arabisdopsis thalia
271	6	4.4	164	21	AAV57149	Arabisdopsis thalia	344	6	4.4	321	20	AAV35152	Amino acid sequenc
272	6	4.4	165	21	AAV60965	Arabisdopsis thalia	345	6	4.4	324	22	AAV60292	C glutamicum prote
273	6	4.4	165	21	AAV50453	Arabisdopsis thalia	346	6	4.4	330	20	AAV88339	Salmonella enteric
274	6	4.4	175	17	AAV87507	Caenorhabditis ele	347	6	4.4	332	20	AAV88068	Streptococcus pyog
275	6	4.4	175	21	AAV43519	Human cancer assoc	348	6	4.4	335	21	AAV95073	Candida albicans p
276	6	4.4	178	21	AAV71064	Human membrane tra	349	6	4.4	335	22	AAV65002	Shrimp white spot
277	6	4.4	178	22	AAV81898	Amino acid sequenc	350	6	4.4	338	19	AAV60521	Kurtlia sp. DTB sy
278	6	4.4	179	21	AAV58304	Arabisdopsis thalia	351	6	4.4	338	22	AAV60651	C glutamicum prote
279	6	4.4	189	22	AAV31900	Amino acid sequenc	352	6	4.4	345	15	AAV51848	Influenza type B H
280	6	4.4	191	21	AAV58303	Arabisdopsis thalia	353	6	4.4	345	15	AAV51849	Influenza type B H
281	6	4.4	193	22	AAV81896	Amino acid sequenc	354	6	4.4	345	15	AAV51850	Influenza type B H
282	6	4.4	193	22	AAV81901	Amino acid sequenc	355	6	4.4	345	15	AAV51851	Influenza type B H
283	6	4.4	193	22	AAV81902	Amino acid sequenc	356	6	4.4	345	15	AAV51852	Influenza type B H
284	6	4.4	193	22	AAV81903	Amino acid sequenc	357	6	4.4	345	15	AAV51853	Influenza type B H
285	6	4.4	193	22	AAV81904	Amino acid sequenc	358	6	4.4	345	15	AAV51854	Influenza type B H
286	6	4.4	193	22	AAV81928	Amino acid sequenc	359	6	4.4	345	15	AAV51855	Influenza type B H
287	6	4.4	196	21	AAV658302	Arabisdopsis thalia	360	6	4.4	345	15	AAV51856	Influenza type B H
288	6	4.4	200	22	AAV81899	Amino acid sequenc	361	6	4.4	345	15	AAV51857	Influenza type B H
289	6	4.4	202	21	AAV636223	Arabisdopsis thalia	362	6	4.4	345	15	AAV51859	Influenza type B H
290	6	4.4	213	21	AAV605867	Arabisdopsis thalia	363	6	4.4	347	15	AAV51845	Influenza type B H
291	6	4.4	221	22	AAV30556	A wild type rat 11	364	6	4.4	347	15	AAV51846	Influenza type B H
292	6	4.4	221	22	AAV30557	A mutagenised rat	365	6	4.4	347	15	AAV51847	Influenza type B H
293	6	4.4	221	22	AAV30558	A mutagenised rat	366	6	4.4	347	15	AAV51858	Influenza type B H
294	6	4.4	221	22	AAV30559	A mutagenised rat	367	6	4.4	351	21	AAV18970	Amino acid sequenc
295	6	4.4	221	22	AAV30560	A mutagenised rat	368	6	4.4	351	22	AAV36685	Human colon cancer
296	6	4.4	221	22	AAV30561	A mutagenised rat	369	6	4.4	353	22	AAV65406	C glutamicum prote
297	6	4.4	221	22	AAV30562	A mutagenised rat	370	6	4.4	360	22	AAV60362	Human polyepitide
298	6	4.4	221	22	AAV30563	A mutagenised rat	371	6	4.4	364	22	AAV39861	Human protein sequ
299	6	4.4	221	22	AAV30564	A mutagenised rat	372	6	4.4	364	22	AAV57714	Corynebacterium gl
300	6	4.4	221	22	AAV30565	A mutagenised rat	373	6	4.4	364	22	AAV79284	Zea mays protein f
301	6	4.4	228	21	AAV57750	Toxoplasma gondii	374	6	4.4	365	21	AAV54549	Human protein sequ
302	6	4.4	229	13	AAV21613	UCH-L3 protein. H	375	6	4.4	365	22	AAV94163	Human colon cancer
303	6	4.4	230	20	AAV9788		376	6	4.4	367	22	AAV75041	

377	6	4.4	370	22	AAW41547	Human polypeptide	450	6	4.4	489	20	AAV26065	Para-Nitrobenzyl E
378	6	4.4	372	22	AAW81006	HIV protease and r	451	6	4.4	496	20	AAV73823	Human prostatic tum
379	6	4.4	372	22	AAW81023	HIV protease and r	452	6	4.4	499	22	AAW40963	Human polypeptide
380	6	4.4	373	22	AAW81049	HIV protease and r	453	6	4.4	499	22	AAW82251	Rat insulin-respon
381	6	4.4	374	21	AAW21092	Modified Treponema	454	6	4.4	503	20	AAV00189	Enterococcus faec
382	6	4.4	374	22	AAW83001	S. epidermidis ope	455	6	4.4	503	21	AAW25432	Arabisopsis thallia
383	6	4.4	376	18	AAW32863	Saccharopolyspora	456	6	4.4	506	21	AAW95594	Arabisopsis thallia
384	6	4.4	376	20	AAW32054	Bovine pregnancy a	457	6	4.4	506	17	AAW97571	Arabisopsis thallia
385	6	4.4	398	12	AAW15614	Human type II inte	458	6	4.4	513	20	AAW18187	Plasmodium falci
386	6	4.4	398	14	AAW42061	Lymphoblastoid der	459	6	4.4	513	20	AAW05897	Vicia sativa omega
387	6	4.4	398	15	AAW60617	Human type II IL-1	460	6	4.4	515	21	AAW46671	Arabisopsis thallia
388	6	4.4	398	16	AAW85480	Human type II inte	461	6	4.4	527	21	AAW48371	Arabisopsis thallia
389	6	4.4	398	19	AAW59267	Human type II IL-1	462	6	4.4	535	21	AAW25431	Arabisopsis thallia
390	6	4.4	398	21	AAW37792	Human interleukin-	463	6	4.4	535	21	AAW28064	Arabisopsis thallia
391	6	4.4	398	22	AAW24185	Human EST encoded	464	6	4.4	537	21	AAW44498	Arabisopsis thallia
392	6	4.4	398	22	AAW50081	Human IL-1R type I	465	6	4.4	538	19	AAW47001	Glutathione-S-tran
393	6	4.4	410	22	AAW86456	S. pneumoniae fibB	466	6	4.4	538	19	AAW44248	Arabisopsis thallia
394	6	4.4	415	14	AAW32922	AAW-1. Homo sapi	467	6	4.4	547	22	AAW50670	C. elegans UNC-5 p
395	6	4.4	415	16	AAW66773	N-terminally trunc	468	6	4.4	551	19	AAW14457	Arabisopsis thallia
396	6	4.4	415	18	AAW33692	Treponema pallidum	469	6	4.4	551	19	AAW59933	Modified T. pallid
397	6	4.4	415	19	AAW68498	Treponema pallidum	470	6	4.4	554	21	AAW36165	Arabisopsis thallia
398	6	4.4	415	19	AAW59930	Modified T. pallid	471	6	4.4	569	20	AAW16102	Acetobacter xyliu
399	6	4.4	426	16	AAW66776	Cell adhesion prot	472	6	4.4	585	18	AAW01671	Influenza B/Panama
400	6	4.4	434	19	AAW59934	Wild type T. palli	473	6	4.4	585	20	AAW75443	Influenza virus B/
401	6	4.4	440	21	AAW28066	Arabisopsis thalia	474	6	4.4	585	22	AAW04953	Influenza virus B/
402	6	4.4	441	21	AAW14499	Arabisopsis thalia	475	6	4.4	586	18	AAW01675	Influenza virus B/
403	6	4.4	443	15	AAW58637	Treponema pallidum	476	6	4.4	586	20	AAW75447	Influenza virus B/
404	6	4.4	443	18	AAW35744	Treponema pallidum	477	6	4.4	586	22	AAW04957	Influenza virus B/
405	6	4.4	453	21	AAW25433	Arabisopsis thalia	478	6	4.4	589	18	AAW01672	Influenza B/Nether
406	6	4.4	456	18	AAW33693	Nucleic acid-bound	479	6	4.4	589	22	AAW75444	Influenza virus B/
407	6	4.4	457	21	AAW28065	Arabisopsis thalia	480	6	4.4	589	22	AAW04954	Influenza virus B/
408	6	4.4	461	19	AAW70964	Human IkaroS isoto	481	6	4.4	591	20	AAW97384	Influenza virus B/
409	6	4.4	468	21	AAW51824	Human OSB protein	482	6	4.4	592	18	AAW01674	Influenza A/Shanha
410	6	4.4	470	10									

523	6	4.4	1008	22	AA882247	Rat insulin-respon	596	5	3.7	8	18	AAW36925	Peptide epitope 20
524	6	4.4	1024	21	AA642350	Arabidopsis thalia	597	5	3.7	9	18	AAW36926	Peptide epitope 21
525	6	4.4	1036	21	AA631888	Arabidopsis thalia	598	5	3.7	9	20	AAAY40779	S6 derivative #11,
526	6	4.4	1055	16	AA870114	IL-1Ryptei-GBP 13	599	5	3.7	9	21	AAAB45561	Human B99-1 HLA B*
527	6	4.4	1055	22	AAW39198	Human polypeptide	600	5	3.7	9	21	AAAB30117	Scaffold protein S
528	6	4.4	1056	22	AAE01980	Human ATPase-relat	601	5	3.7	9	21	AAAB30118	Scaffold protein S
529	6	4.4	1070	21	AA631887	Arabidopsis thalia	602	5	3.7	9	21	AAAB6786	Telemorse peptide
530	6	4.4	1074	20	AAV00206	Enterococcus faeca	603	5	3.7	9	22	AAW23310	HIV peptide SEQ ID
531	6	4.4	1074	20	AAV00188	Enterococcus faeca	604	5	3.7	10	20	AAW84235	Antigenic peptide
532	6	4.4	1096	21	AA648592	Arabidopsis thalia	605	5	3.7	10	20	AAW84236	Antigenic peptide
533	6	4.4	1096	21	AA848833	Amino acid sequenc	606	5	3.7	10	22	AA695753	Saccharomyces cere
534	6	4.4	1105	21	AA642349	Arabidopsis thalia	607	5	3.7	10	22	AA686101	Saccharomyces cere
535	6	4.4	1120	20	AAV00641	Telemorse protein	608	5	3.7	10	22	AAAB48575	Human MO-Bc-203 de
536	6	4.4	1120	20	AAV00650	Telemorse (ver. 2	609	5	3.7	11	16	AAW21464	Schistosoma elasta
537	6	4.4	1130	21	AA648591	Arabidopsis thalia	610	5	3.7	11	16	AAAB19278	A ricin toxin A ch
538	6	4.4	1132	19	AAW71376	Human telomerase c	611	5	3.7	11	22	AAAB66304	Murine derived ant
539	6	4.4	1132	19	AAW46957	Human telomerase r	612	5	3.7	11	22	AAAB50076	Csk tyrosine kinas
540	6	4.4	1132	19	AAW56113	Human telomerase r	613	5	3.7	12	15	AAAB67139	Factor VIIa deri
541	6	4.4	1132	20	AAV43621	A human telomerase	614	5	3.7	12	18	AAW33289	Peptide 8 used in
542	6	4.4	1132	20	AAV28861	Human telomerase r	615	5	3.7	12	22	AAU05218	Zinc finger protei
543	6	4.4	1132	20	AAV32090	Human telomerase r	616	5	3.7	12	22	AAAB49264	Zinc finger helica
544	6	4.4	1132	20	AAV28401	Human EST2 protein	617	5	3.7	13	18	AAW99278	Peptide C1 from WO
545	6	4.4	1132	20	AAV26580	Human telomerase r	618	5	3.7	13	18	AAW33288	Peptide 7 used in
546	6	4.4	1132	20	AAV00627	Human telomerase p	619	5	3.7	14	15	AAAB3343	Chimeric human Ab
547	6	4.4	1132	20	AAV00638	Truncated telomera	620	5	3.7	14	18	AAW99277	Peptide C0 from WO
548	6	4.4	1132	21	AAW90251	Human catalytic te	621	5	3.7	14	18	AAW33287	Peptide 6 used in
549	6	4.4	1132	21	AAV96566	hEST2, a human tel	622	5	3.7	14	21	AAAB01630	Chimeric immunogl
550	6	4.4	1132	22	AAAB9930	Human telomerase p	623	5	3.7	14	21	AAV65739	Breast cancer susc
551	6	4.4	1132	22	AA643329	Human protein #2.	624	5	3.7	15	10	AAAP91741	Antigenic C-termin
552	6	4.4	1132	22	AA648859	Heart muscle cell	625	5	3.7	15	14	AAAB33253	PKM61HR3 derived
553	6	4.4	1140	22	AAAB50669	C. elegans UNC-5 p	626	5	3.7	15	14	AAAB65528	Heavy chain variab
554	6	4.4	1144	22	AAAB59293	Human polypeptide	627	5	3.7	16	15	AAAB5150	CS134-149 ("S1").
555	6	4.4	1150	19	AAW47006	Glutathione-S-tran	628	5	3.7	16	18	AAW40945	Cryptic peptide 2.
556	6	4.4	1154	19	AAW61350	Human telomerase p	629	5	3.7	16	20	AAV25535	Human MHC Class II
557	6	4.4	1165	22	AAW39312	Human polypeptide	630	5	3.7	17	21	AAAB28948	Peptide Fel 33.. F
558	6	4.4	1166	20	AAV00647	Telemorse (ver. 2	631	5	3.7	17	21	AAV87689	Feline human TRFP
559	6	4.4	1177	22	AAW41079	Human polypeptide	632	5	3.7	17	21	AAV90119	Cat TRFP derived p
560	6	4.4	1177	22	AAW41098	Human polypeptide	633	5	3.7	17	21	AAV51486	Human TRFP derived
561	6	4.4	1189	19	AAW47008	Glutathione-S-tran	634	5	3.7	17	22	AAAB9408	Staphylokinase Sak
562	6	4.4	1189	21	AA642348	Arabidopsis thalia	635	5	3.7	17	22	AAAB9409	Staphylokinase Sak
563	6	4.4	1244	19	AAW59358	Human retinal dege	636	5	3.7	17	22	AAAB89090	Chimeric L6-VH plu
564	6	4.4	1270	22	AAE01982	Human ATPase-relat	637	5	3.7	18	21	AAAB28949	Peptide Fel 34.. F
565	6	4.4	1276	21	AA631886	Arabidopsis thalia	638	5	3.7	18	21	AAV87690	Feline human TRFP
566	6	4.4	1285	19	AAW47000	HIS tagged thio	639	5	3.7	18	21	AAV90120	Cat TRFP derived p
567	6	4.4	1294	20	AAV39653	Zea mays Rpg1-2 pr	640	5	3.7	18	21	AAV51487	Human TRFP derived
568	6	4.4	1336	21	AA648590	Arabidopsis thalia	641	5	3.7	18	21	AAV59134	Yeast STE20 GBD/CR
569	6	4.4	1354	18	AAW23654	Physiologically ac	642	5	3.7	18	22	AAAB20421	Anti-FIX/FTXa anti
570	6	4.4	1354	19	AAW71020	A modified Rho tar	643	5	3.7	19	13	AAAB26956	Human T lymphocyte
571	6	4.4	1354	20	AAV07082	Renal cancer assoc	644	5	3.7	19	16	AAAB80836	Human CD40 ligand
572	6	4.4	1405	19	AAW56101	Enhanced green flu	645	5	3.7	19	17	AAW49182	Human leucocyte an
573	6	4.4	1426	22	AAE01984	Human ATPase-relat	646	5	3.7	19	18	AAW16904	Helicobacter pylor
574	6	4.4	1456	22	AAAB61995	Rat peripheral ner	647	5	3.7	19	18	AAW16905	Helicobacter pylor
575	6	4.4	1957	18	AAW21740	Variant rat DRG (S	648	5	3.7	19	20	AAW78360	MAM mitogenic acti
576	6	4.4	1957	18	AAW21737	Wild type rat DRG	649	5	3.7	19	21	AAV70296	Plasmodium falcipa
577	6	4.4	2132	18	AAW21739	Variant rat DRG (S	650	5	3.7	19	22	AAW5085	Peptide #1519 enco
578	6	4.4	2206	21	AAAB18254	Plasmodium falcipa	651	5	3.7	19	22	AAW27533	Peptide #1570 enco
579	6	4.4	2485	21	AAAB18172	Plasmodium falcipa	652	5	3.7	19	22	AAW02821	Peptide #1503 enco
580	6	4.4	2841	21	AAAB01581	Protein encoded by	653	5	3.7	20	19	AAW00690	Rhodococcus haloal
581	6	4.4	3079	15	AAAB59926	GAP protein Irax2.	654	5	3.7	20	19	AAW76178	Feline FlAP40 pro
582	6	4.4	3519	21	AAV92709	S. anthiocticus 8,	655	5	3.7	20	21	AAV45069	D. immitis aromati
583	6	4.4	4150	21	AAV92707	S. anthiocticus 8,	656	5	3.7	20	22	AAAB68950	Arabidopsis thalia
584	6	4.4	5701	22	AAW05328	Peptide #4010 enco	657	5	3.7	21	15	AAAB6969	J alpha sequence (
585	6	4.4	26926	22	AAU05396	Human filin (cone	658	5	3.7	21	18	AAW35466	Immunogenic agent
586	5	3.7		5	AAW51489	Peptide epitope 15	659	5	3.7	21	21	AAAB28965	Peptide encoded by
587	5	3.7		6	AAW36920	Pre-sequence which	660	5	3.7	21	21	AAV87709	Feline human TRFP
588	5	3.7		6	AAW51524	Pre-sequence which	661	5	3.7	21	21	AAV90135	TRFP derived pepit
589	5	3.7		6	AAW51526	Pre-sequence which	662	5	3.7	21	21	AAV51506	Human TRFP derived
590	5	3.7		6	AAW51536	Pre-sequence which	663	5	3.7	22	16	AAAB83834	Silkworm phenoloxi
591	5	3.7		6	AAW51537	Pre-sequence which	664	5	3.7	22	20	AAV19196	Lecithin:cholester
592	5	3.7		7	AAW94561	GL-7ACA acylase al	665	5	3.7	22	20	AAV18942	Lecithin:cholester
593	5	3.7		7	AAW36924	Peptide epitope 19	666	5	3.7	22	20	AAV18688	Lecithin:cholester
594	5	3.7		7	AAW06506	DPPIV peptide frag	667	5	3.7	22	20	AAV18425	Lecithin:cholester
595	5	3.7		7	AAAB5436	Serum DPPIV trypti	668	5	3.7	22	20	AAW83093	Peptide from the 3

669	5	3.7	22	21	AAV77782	Core polypeptide u	742	5	3.7	27	22	AAAI4219	Peptide #653 encod
670	5	3.7	22	22	AAAI1980	Peptide #6017 enco	743	5	3.7	27	22	AAAI20818	Peptide #7252 enco
671	5	3.7	22	22	AAAB78467	Core polypeptide #	744	5	3.7	27	22	AAAI26629	Peptide #666 encod
672	5	3.7	23	15	AAAR46968	Core polypeptide #	745	5	3.7	27	22	AAAI36274	Peptide #10311 enc
673	5	3.7	23	19	AAAS6706	Cytotoxic lymphocy	746	5	3.7	27	22	AAAI01951	Peptide #633 encod
674	5	3.7	23	21	AAV96435	Mutant human TGF-b	747	5	3.7	28	19	AAAI46283	Moraxella catartha
675	5	3.7	23	21	AAV83620	Peptide fragment o	748	5	3.7	28	20	AAV29691	Moraxella catartha
676	5	3.7	23	21	AAV77779	Core polypeptide u	749	5	3.7	29	21	AAV51912	Basic peptide NST3
677	5	3.7	23	21	AAV77780	Core polypeptide u	750	5	3.7	29	21	AAV83795	Ationic-phospholip
678	5	3.7	23	21	AAV77781	Core polypeptide u	751	5	3.7	30	19	AAV77620	Staphylococcus aur
679	5	3.7	23	21	AAV77783	Core polypeptide u	752	5	3.7	31	21	AAV83798	Ationic-phospholip
680	5	3.7	23	21	AAV77784	Core polypeptide u	753	5	3.7	32	9	AAAB80106	Encoded by Staphyl
681	5	3.7	23	21	AAV89820	Core polypeptide f	754	5	3.7	32	21	AAAB38146	Human secreted pro
682	5	3.7	23	21	AAV89821	Core polypeptide f	755	5	3.7	33	17	AAAB95174	Stem cell factor C
683	5	3.7	23	21	AAV65740	Breast cancer susc	756	5	3.7	33	21	AAAB16943	Bacteriophage Dp-1
684	5	3.7	23	22	AAAB78221	Core polypeptide T	757	5	3.7	33	21	AAV89720	Core polypeptide f
685	5	3.7	23	22	AAAB78222	Core polypeptide T	758	5	3.7	33	21	AAV89721	Core polypeptide f
686	5	3.7	23	22	AAAB78464	Core polypeptide #	759	5	3.7	33	22	AAAB78121	Core polypeptide T
687	5	3.7	23	22	AAAB78465	Core polypeptide #	760	5	3.7	33	22	AAAB78122	Core polypeptide T
688	5	3.7	23	22	AAAB78466	Core polypeptide #	761	5	3.7	34	21	AAV83796	Ationic-phospholip
689	5	3.7	23	22	AAAB78468	Core polypeptide #	762	5	3.7	34	22	AAAI89944	Peptide #5378 enco
690	5	3.7	23	22	AAAB78469	Core polypeptide #	763	5	3.7	34	22	AAAI28826	Peptide #2863 enco
691	5	3.7	24	12	AAAI3011	Human Factor VIII (764	5	3.7	34	22	AAAI31520	Peptide #5557 enco
692	5	3.7	24	21	AAV65741	Breast cancer susc	765	5	3.7	34	22	AAU05883	Cone snail O-supe
693	5	3.7	24	22	AAAI6861	Peptide #6115 enco	766	5	3.7	34	22	AAAI04069	Peptide #2751 enco
694	5	3.7	24	22	AAAI3910	Peptide #6947 enco	767	5	3.7	35	14	AAAI45158	Botriocetin one-cha
695	5	3.7	25	19	AAAI5051	Pept2 tryptic pepti	768	5	3.7	35	21	AAAB44354	Human secreted pro
696	5	3.7	25	22	AAAI1991	Peptide #6425 enco	769	5	3.7	35	21	AAV88649	Hybrid polypeptide
697	5	3.7	25	22	AAAI3693	Peptide #7730 enco	770	5	3.7	35	21	AAV89717	Core polypeptide f
698	5	3.7	26	14	AAAR36544	Peptide 2, Felis,	771	5	3.7	35	21	AAV89730	Core polypeptide f
699	5	3.7	26	14	AAAR41977	Human T cell react	772	5	3.7	35	21	AAV89774	Core polypeptide f
700	5	3.7	26	15	AAAR52478	Human heavy chain	773	5	3.7	35	21	AAV89792	Core polypeptide f
701	5	3.7	26	15	AAAR52480	Human heavy chain	774	5	3.7	35	21	AAV89799	Core polypeptide f
702	5	3.7	26	15	AAAR52462	Human heavy chain	775	5	3.7	35	21	AAV89800	Core polypeptide f
703	5	3.7	26	15	AAAR52463	Human heavy chain	776	5	3.7	35	22	AAAB68863	Core polypeptide #
704	5	3.7	26	15	AAAR52466	Human heavy chain	777	5	3.7	35	22	AAAB78118	Core polypeptide T
705	5	3.7	26	15	AAAR52474	Human heavy chain	778	5	3.7	35	22	AAAB78131	Core polypeptide T
706	5	3.7	26	15	AAAR52475	Human heavy chain	779	5	3.7	35	22	AAAB78173	Core polypeptide T
707	5	3.7	26	15	AAAR52476	Human heavy chain	780	5	3.7	35	22	AAAB78193	Core polypeptide T
708	5	3.7	26	15	AAAR52453	Human heavy chain	781	5	3.7	35	22	AAAB78200	Core polypeptide T
709	5	3.7	26	15	AAAR52455	Human heavy chain	782	5	3.7	35	22	AAAB78201	Core polypeptide T
710	5	3.7	26	15	AAAR52456	Human heavy chain	783	5	3.7	36	12	AAAR12372	Antihaemostatic pe
711	5	3.7	26	15	AAAR52458	Human heavy chain	784	5	3.7	36	20	AAV35985	Extended human sec
712	5	3.7	26	15	AAAR52289	Mouse heavy chain	785	5	3.7	36	21	AAV88688	Core polypeptide f
713	5	3.7	26	15	AAAR52290	Mouse heavy chain	786	5	3.7	36	21	AAV89689	Core polypeptide f
714	5	3.7	26	15	AAAR52298	Mouse heavy chain	787	5	3.7	36	22	AAAI14672	Peptide #1106 enco
715	5	3.7	26	15	AAAR52273	Mouse heavy chain	788	5	3.7	36	22	AAAI27091	Peptide #1128 enco
716	5	3.7	26	15	AAAR52276	Mouse heavy chain	789	5	3.7	36	22	AAAI02395	Peptide #1077 enco
717	5	3.7	26	15	AAAR52277	Mouse heavy chain	790	5	3.7	36	22	AAAB20035	Zinc finger helica
718	5	3.7	26	15	AAAR52278	Mouse heavy chain	791	5	3.7	36	22	AAAB78089	Core polypeptide T
719	5	3.7	26	15	AAAR52279	Mouse heavy chain	792	5	3.7	36	22	AAAB78090	Core polypeptide T
720	5	3.7	26	15	AAAR52281	Mouse heavy chain	793	5	3.7	36	22	AAAB59477	Human secreted pro
721	5	3.7	26	15	AAAR52282	Mouse heavy chain	794	5	3.7	36	20	AAAB88395	Human znenu1 epitop
722	5	3.7	26	15	AAAR52283	Mouse heavy chain	795	5	3.7	37	21	AAAB63167	Human secreted pro
723	5	3.7	26	15	AAAR52260	Mouse heavy chain	796	5	3.7	37	21	AAAB45268	Human secreted pro
724	5	3.7	26	15	AAAR52261	Mouse heavy chain	797	5	3.7	37	21	AAV89732	Core polypeptide f
725	5	3.7	26	15	AAAR52262	Mouse heavy chain	798	5	3.7	37	22	AAAI19949	Peptide #6383 enco
726	5	3.7	26	15	AAAR52263	Mouse heavy chain	799	5	3.7	37	22	AAAI36011	Peptide #7638 enco
727	5	3.7	26	15	AAAR52264	Mouse heavy chain	800	5	3.7	37	22	AAAB78133	Core polypeptide T
728	5	3.7	26	15	AAAR52266	Mouse heavy chain	801	5	3.7	37	22	AAAB65949	Human secreted pro
729	5	3.7	26	15	AAAR52267	Mouse heavy chain	802	5	3.7	38	21	AAV89765	Core polypeptide f
730	5	3.7	26	15	AAAR52268	Mouse heavy chain	803	5	3.7	39	20	AAV29882	Ahesion epitope N
731	5	3.7	26	15	AAAR52269	Mouse heavy chain	804	5	3.7	39	21	AAAB57001	Human prostate can
732	5	3.7	26	15	AAAR52270	Mouse heavy chain	805	5	3.7	39	21	AAV89731	Core polypeptide f
733	5	3.7	26	19	AAAI6253	Moraxella catartha	806	5	3.7	39	21	AAV89744	Core polypeptide f
734	5	3.7	26	19	AAAI6256	Moraxella catartha	807	5	3.7	39	21	AAV89745	Core polypeptide f
735	5	3.7	26	21	AAAB28943	Peptide 2 derived	808	5	3.7	39	21	AAV89748	Core polypeptide f
736	5	3.7	26	21	AAAB18497	Peptide substrate	809	5	3.7	39	21	AAV89766	Core polypeptide f
737	5	3.7	26	21	AAV87684	Feline human TRFP	810	5	3.7	39	22	AAAB78132	Core polypeptide T
738	5	3.7	26	21	AAV90109	Cat TRFP derived p	811	5	3.7	39	22	AAAB78145	Core polypeptide T
739	5	3.7	26	21	AAV83797	Antonic-phospholip	812	5	3.7	39	22	AAAB78146	Core polypeptide T
740	5	3.7	26	21	AAV51481	Human TRFP derived	813	5	3.7	39	22	AAAB78149	Core polypeptide T
741	5	3.7	27	19	AAV86016	S. pneumoniae deri	814	5	3.7	39	22	AAAB78166	Core polypeptide T

815	5	3.7	39	22	AAB78167	Core polypeptide T	888	5	3.7	55	20	AAV02669	Human secreted pro
816	5	3.7	40	17	AAR96936	Thymosin beta 14.	889	5	3.7	55	21	AAB34671	Gene 35 human secr
817	5	3.7	40	21	AAB38431	Fragment of human	890	5	3.7	55	21	AAB34672	Human secreted pro
818	5	3.7	40	21	AAB12944	Neurotransmission	891	5	3.7	55	21	AAAG24546	Arabidopsis thalia
819	5	3.7	40	21	AAV80271	Thymosin beta 4 pe	892	5	3.7	56	22	AAM18283	Peptide #4717 enco
820	5	3.7	40	21	AAV89747	Core polypeptide f	893	5	3.7	56	22	AAAM30773	Peptide #4810 enco
821	5	3.7	40	22	AAB78148	Core polypeptide T	894	5	3.7	56	22	AAAM36305	Peptide #10342 enc
822	5	3.7	41	19	AAW53674	FIV pPR clone 34 O	895	5	3.7	56	22	AAAM05896	Peptide #4578 enco
823	5	3.7	41	20	AAV12877	Human 5' EST secre	896	5	3.7	56	22	AAAG73383	Human gene 2-encod
824	5	3.7	41	21	AAV89749	Core polypeptide f	897	5	3.7	57	22	AAB81179	Chimeric transgult
825	5	3.7	41	22	AAAM15285	Peptide #1719 enco	898	5	3.7	57	21	AAAG14328	Arabidopsis thalia
826	5	3.7	41	22	AAU06521	Human CYP2B6 prote	899	5	3.7	57	21	AAAG54611	Zea mays protein f
827	5	3.7	41	22	AAU06522	Human CYP2B6 prote	900	5	3.7	57	22	AAAM15951	Peptide #2385 enco
828	5	3.7	41	22	AAB81172	Transglutaminase r	901	5	3.7	57	22	AAAM20678	Peptide #7112 enco
829	5	3.7	41	22	AAB81177	Modified transgult	902	5	3.7	57	22	AAAM28454	Peptide #2491 enco
830	5	3.7	41	22	AAB81178	Modified transgult	903	5	3.7	57	22	AAAM34808	Peptide #8845 enco
831	5	3.7	41	22	AAB78150	Core polypeptide T	904	5	3.7	57	22	AAAM35838	Peptide #9875 enco
832	5	3.7	42	21	AAV89746	Core polypeptide f	905	5	3.7	57	22	AAAM36456	Peptide #10493 enc
833	5	3.7	42	22	AAAM14962	Peptide #1336 enco	906	5	3.7	57	22	AAAM03689	Peptide #2371 enco
834	5	3.7	42	22	AAAM27396	Peptide #1370 enco	907	5	3.7	58	17	AAW34239	SH3 domain of huma
835	5	3.7	42	22	AAAM02688	Core polypeptide T	908	5	3.7	58	19	AAW38588	Streptococcus pneu
836	5	3.7	42	22	AAAB78147	Transglutaminase r	909	5	3.7	58	21	AAW53983	Human colon cancer
837	5	3.7	43	16	AAR70973	HARDS virus peptid	910	5	3.7	58	21	AAAG09957	Arabidopsis thalia
838	5	3.7	43	17	AAAR95471	v44, monoclonal an	911	5	3.7	58	21	AAAG40074	Arabidopsis thalia
839	5	3.7	43	19	AAW63984	Yeast tropomyosin	912	5	3.7	58	21	AAAG59902	Arabidopsis thalia
840	5	3.7	43	21	AAV86370	Human gene 11-enco	913	5	3.7	58	21	AAAG03445	Human secreted pro
841	5	3.7	43	22	AAAM33104	Peptide #7141 enco	914	5	3.7	58	22	AAAM23685	Human EST encoded
842	5	3.7	43	22	AAAG74160	Human colon cancer	915	5	3.7	58	22	AAE01280	Human gene 11 enco
843	5	3.7	43	22	AAB81171	Transglutaminase r	916	5	3.7	59	22	AAE17863	Peptide #4297 enco
844	5	3.7	44	16	AAAR83836	Silkworm prophenol	917	5	3.7	59	22	AAAM30370	Peptide #4407 enco
845	5	3.7	44	20	AAV74023	Human prostate tum	918	5	3.7	60	21	AAAB34380	Gene 14 human secr
846	5	3.7	44	21	AAAB43473	Human cancer assoc	919	5	3.7	60	21	AAAB34381	Human secreted pro
847	5	3.7	44	21	AAV80272	Thymosin beta 4 pe	920	5	3.7	60	21	AAAG16411	Arabidopsis thalia
848	5	3.7	44	22	AAB81173	Transglutaminase r	921	5	3.7	60	22	AAAM15955	Peptide #2389 enco
849	5	3.7	45	16	AAR74269	Borrelia OspC SSAL	922	5	3.7	60	22	AAAM17151	Peptide #3585 enco
850	5	3.7	45	18	AAW36056	Human thymosin bet	923	5	3.7	60	22	AAAM28457	Peptide #2494 enco
851	5	3.7	45	18	AAAM14281	Human neuroblastom	924	5	3.7	60	22	AAAM29134	Peptide #3171 enco
852	5	3.7	45	19	AAW68573	Rat thymosin-beta1	925	5	3.7	60	22	AAAM29643	Peptide #3680 enco
853	5	3.7	45	19	AAW72683	Ikaros protein SEQ	926	5	3.7	60	22	AAAM03693	Peptide #2375 enco
854	5	3.7	45	19	AAW46486	Human thymosin bet	927	5	3.7	60	22	AAAM04366	Peptide #3048 enco
855	5	3.7	45	19	AAW44275	Human thymosin bet	928	5	3.7	60	22	AAAM04846	Peptide #3528 enco
856	5	3.7	45	20	AAV33663	Streptoveritciliu	929	5	3.7	61	15	AAAR66849	Rice mitochondrial
857	5	3.7	45	20	AAV13083	Human secreted pro	930	5	3.7	61	15	AAAR74751	Rice mitochondrial
858	5	3.7	45	21	AAAG06157	Arabidopsis thalia	931	5	3.7	62	14	AAAR38495	B. nodosus pillin P
859	5	3.7	45	21	AAV76812	Human thymosin bet	932	5	3.7	62	22	AAAM19687	Peptide #6121 enco
860	5	3.7	45	22	AAAM14966	Peptide #1400 enco	933	5	3.7	62	22	AAAM22046	Peptide #8480 enco
861	5	3.7	45	22	AAAM27400	Peptide #1437 enco	934	5	3.7	62	22	AAAM32928	Peptide #6965 enco
862	5	3.7	45	22	AAB81159	Pre-pro transgluta	935	5	3.7	62	22	AAAM38427	Peptide #12464 enc
863	5	3.7	45	22	AAB81175	Modified transgult	936	5	3.7	63	22	AAAM14318	Peptide #752 encod
864	5	3.7	45	22	AAB81176	Modified transgult	937	5	3.7	63	22	AAAM26728	Peptide #765 encod
865	5	3.7	46	12	AAAR10755	Non-A non-B heptai	938	5	3.7	63	22	AAAM02047	Peptide #729 encod
866	5	3.7	47	22	AAAM21200	Peptide #7634 enco	939	5	3.7	63	22	AAU02804	Taxus cuspidata RT
867	5	3.7	47	22	AAAM37417	Peptide #11454 enco	940	5	3.7	64	22	AAAM15723	Peptide #2157 enco
868	5	3.7	48	22	AAAM35360	Peptide #9397 enco	941	5	3.7	64	22	AAAM28228	Peptide #2265 enco
869	5	3.7	49	21	AAAG20089	Arabidopsis thalia	942	5	3.7	64	22	AAAM33125	Peptide #5462 enco
870	5	3.7	50	20	AAV12009	Human 5' EST secre	943	5	3.7	64	22	AAAM03457	Peptide #2139 enco
871	5	3.7	50	21	AAB39098	Human secreted pro	944	5	3.7	64	22	AAE01816	Human gene 10 enco
872	5	3.7	50	21	AAAG56198	Arabidopsis thalia	945	5	3.7	65	21	AAAG55992	Arabidopsis thalia
873	5	3.7	50	22	AAAM35311	Peptide #9348 enco	946	5	3.7	65	22	AAAM15961	Peptide #2395 enco
874	5	3.7	51	22	AAAM20000	Peptide #6434 enco	947	5	3.7	65	22	AAAM28463	Peptide #2500 enco
875	5	3.7	51	22	AAAM35719	Peptide #7736 enco	948	5	3.7	65	22	AAAM03698	Peptide #2380 enco
876	5	3.7	51	22	AAAM34869	Peptide #8906 enco	949	5	3.7	65	22	AAAG81287	Human ARP protein
877	5	3.7	52	20	AAV60333	Human normal blad	950	5	3.7	66	21	AAAB34637	Gene 3 human secre
878	5	3.7	52	21	AAAG46287	Arabidopsis thalia	951	5	3.7	66	22	AAAB34638	Human secreted pro
879	5	3.7	52	21	AAAG57145	Arabidopsis thalia	952	5	3.7	66	22	AAAM20089	Peptide #6523 enco
880	5	3.7	52	22	AAAM37794	Peptide #11831 enc	953	5	3.7	66	22	AAAM33953	Peptide #7990 enco
881	5	3.7	52	22	AAAG75231	Human colon cancer	954	5	3.7	67	14	AAAR38496	B. nodosus pillin P
882	5	3.7	53	21	AAAG58688	Arabidopsis thalia	955	5	3.7	67	21	AAAG59713	Arabidopsis thalia
883	5	3.7	53	22	AAAM34088	Peptide #8125 enco	956	5	3.7	67	21	AAAG59816	Arabidopsis thalia
884	5	3.7	53	22	AAAM34627	Peptide #8664 enco	957	5	3.7	67	22	AAAM17275	Peptide #3709 enco
885	5	3.7	54	20	AAW783358	M arthritis mit	958	5	3.7	67	22	AAAM29773	Peptide #3810 enco
886	5	3.7	54	21	AAV54438	Peptide which mimi	959	5	3.7	67	22	AAAM04963	Peptide #3645 enco
887	5	3.7	54	22	AAAM36386	Peptide #10423 enc	960	5	3.7	68	21	AAAG00889	Human secreted pro

961	5	3.7	68	22	AAB63528	Human gastric canc
962	5	3.7	69	14	AAR38953	LD78 Asp26>Ser. H
963	5	3.7	69	20	AAV33810	Scsmd3-YLR147C a Y
964	5	3.7	69	20	AAV00282	Human secreted pro
965	5	3.7	69	22	AAB65882	Murine TANGO 257.1
966	5	3.7	70	22	AAM32668	Peptide #6705 enco
967	5	3.7	70	22	AAM37123	Peptide #11160 enc
968	5	3.7	71	21	AAB52078	Gene 15 human secr
969	5	3.7	71	21	AAG24493	Arabidopsis thalia
970	5	3.7	71	21	AAG38103	Arabidopsis thalia
971	5	3.7	71	22	AAM18149	Peptide #4583 enco
972	5	3.7	71	22	AAM30652	Peptide #4689 enco
973	5	3.7	72	17	AAR59546	Klebsiella pneumon
974	5	3.7	72	22	AAM31936	Peptide #5973 enco
975	5	3.7	73	22	AAM25239	Human protein sequ
976	5	3.7	73	22	AAM42458	Human kidney relat
977	5	3.7	74	22	AAM24234	Human EST encoded
978	5	3.7	74	22	AAB99901	Human ribosomal pr
979	5	3.7	75	21	AAG24523	Arabidopsis thalia
980	5	3.7	75	21	AAG24969	Arabidopsis thalia
981	5	3.7	75	21	AAG57279	Arabidopsis thalia
982	5	3.7	75	22	AAM20100	Peptide #6534 enco
983	5	3.7	75	22	AAM33974	Peptide #8011 enco
984	5	3.7	75	22	AAM34249	Peptide #8286 enco
985	5	3.7	75	22	AAM42242	Human breast or ov
986	5	3.7	75	22	AAG92784	C glutamic prote
987	5	3.7	76	20	AAV12175	Human 5' EST sece
988	5	3.7	76	21	AAB54024	Human pancreatic c
989	5	3.7	76	21	AAB44881	Human secreted pro
990	5	3.7	76	22	AAB44882	Human secreted pro
991	5	3.7	76	22	AAG76110	Human colon cancer
992	5	3.7	77	21	AAG24492	Arabidopsis thalia
993	5	3.7	77	21	AAG26558	Arabidopsis thalia
994	5	3.7	77	21	AAG26713	Zea mays protein f
995	5	3.7	77	22	AAM14474	Peptide #908 enco
996	5	3.7	77	22	AAM26887	Peptide #924 enco
997	5	3.7	77	22	AAM02301	Peptide #883 enco
998	5	3.7	78	21	AAG38102	Arabidopsis thalia
999	5	3.7	79	20	AAM87979	Ubiquitin-like dom
1000	5	3.7	79	22	AAG76551	Human colon cancer

ALIGNMENTS

RESULT 1
AAM03071 standard; protein; 136 AA.
XX AAM03071;
AC XX
XX
DT 19-FEB-1997 (first entry)
XX
DE Wild-type staphylokinase.
XX
XX Staphylokinase; mutant; mutein; variant; immunogenicity; decrease;
KW derivative; SakSTAR; arterial thrombosis; thrombolytic agent.
XX
XX Staphylococcus aureus.
OS
XX
XX
FH Key Location/Qualifiers
FT Region /label= M20_epitope
FT 5.6
FT Region /label= M21_epitope
FT 8.10
FT Region /label= M21_epitope
FT 11.14
FT Region /label= M1_epitope
FT 19
FT Region /label= M22_epitope
FT 33.35
FT Region /label= M2_epitope
FT 35.38
FT Region /label= M3_epitope
FT

FT	Region	46..50
FT	/label= M4_epitope	
FT	57..59	
FT	Region	
FT	/label= M5_epitope	
FT	61..65	
FT	Region	
FT	/label= M6_epitope	
FT	65..69	
FT	Region	
FT	/label= M7_epitope	
FT	74..77	
FT	Region	
FT	/label= M8_epitope	
FT	80..82	
FT	Region	
FT	/label= M9_epitope	
FT	86..88	
FT	Region	
FT	/label= M10_epitope	
FT	93..94	
FT	Region	
FT	/label= M11_epitope	
FT	96..98	
FT	Region	
FT	/label= M12_epitope	
FT	99..100	
FT	Region	
FT	/label= M13_epitope	
FT	99..102	
FT	Region	
FT	/label= M14_epitope	
FT	108..109	
FT	Region	
FT	/label= M15_epitope	
FT	115..119	
FT	Region	
FT	/label= M16_epitope	
FT	119..121	
FT	Region	
FT	/label= M17_epitope	
FT	130	
FT	Region	
FT	/label= M18_epitope	
FT	134..136	
FT	/label= M19_epitope	
FT	EP21982-A1.	
FT	17-JUL-1996.	
PD	XX	
XX	06-JAN-1995; 95EP-0200023.	
XX	06-JAN-1995; 95EP-0200023.	
XX	06-JAN-1995; 95EP-0200023.	
XX	XX	
PA	(COLL-) COLLEN D J.	
PA	(LEUV-) LEUVEN RES & DEV VZW.	
PI	Collen D;	
PI	XX	
DR	WPI; 1996-322832/33.	
XX	XX	
PT	New staphylokinase mutants with reduced immunogenicity - useful for	
PT	treating arterial thrombosis	
XX	XX	
PS	Disclosure; Page 16; 21pp; English.	
XX	XX	
CC	Staphylokinase derivatives showing a reduced immunogenicity as	
CC	compared to wild-type staphylokinase are claimed. The derivatives	
CC	are useful as thrombolytic agents to treat arterial thrombosis and	
CC	are pref. produced by eliminating at least one of the epitopes	
CC	indicated in the features table. The epitopes are destroyed by	
CC	replacing one or more amino acid residues in a charge cluster by an	
CC	Ala residue. Mutations are introduced using site-directed	
CC	mutagenesis on wild-type staphylokinase genomic DNA from the S.aureus	
CC	lysogenic strain SakSTAR. The present sequence is that of wild-type	
CC	SakSTAR staphylokinase.	
XX	XX	
SO	Sequence 136 AA:	

Query Match 100.0%; Score 136; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.9e-131;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSSFDKRYKKKDDASYPFPGPYLAWVNTGVDKGNELSPHYVEFPIKGTITTKKI 60
|||||

```

Db      1 sssfdkgykkgddasysfeptgpylmvntgyvdskgnellspkgttltketi 60
OY      61 EYVEMALDATATYKKEFRVVELDPSAKIEVYYDKNKKKEETKSPFITEKGFVVPDLSEHI 120
        |||
Db      61 eyvewaldatatykefrvveldpksakievtydknkkkeetksfptekgfvpdlsehi 120
OY      121 KNPGENLITKVVIEKK 136
        |||
Db      121 knpgfnliltkvievkk 136

RESULT 2
AAW03086
ID      AAW03086 standard; protein; 136 AA.
XX
AC      AAW03086;
XX
DT      19-FEB-1997 (first entry)
XX
DE      Wild-type staphylokinase.
XX
KW      Staphylokinase; mutant; mutein; variant; immunogenicity; decrease;
        derivative; SakSTAR; arterial thrombosis; thrombolytic agent.
XX
OS      Staphylococcus aureus.
XX
FH      Key
        Location/Qualifiers
FT      Region
        /label= M20_epitope
        5..6
FT      Region
        /label= M21_epitope
        8..10
FT      Region
        /label= M21_epitope
        11..14
FT      Region
        /label= M1_epitope
        19
FT      Region
        /label= M22_epitope
        33..35
FT      Region
        /label= M2_epitope
        35..38
FT      Region
        /label= M3_epitope
        46..50
FT      Region
        /label= M4_epitope
        57..59
FT      Region
        /label= M5_epitope
        61..65
FT      Region
        /label= M6_epitope
        65..69
FT      Region
        /label= M7_epitope
        74..77
FT      Region
        /label= M8_epitope
        80..82
FT      Region
        /label= M9_epitope
        86..88
FT      Region
        /label= M10_epitope
        93..94
FT      Region
        /label= M11_epitope
        96..98
FT      Region
        /label= M12_epitope
        99..100
FT      Region
        /label= M13_epitope
        99..102
FT      Region
        /label= M14_epitope
        108..109
FT      Region
        /label= M15_epitope
        115..119
FT      Region
        /label= M16_epitope
        119..121
FT      Region
        /label= M17_epitope
        130
FT      Region
        /label= M18_epitope
        134..136
FT      Region
        /label= M19_epitope
        136
XX
PN      W09621016-A2.

```

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XX      11-JUL-1996.
PD
XX      03-JAN-1996; 96WO-EP00081.
PF
XX      17-NOV-1995; 95JP-0299781.
PR      06-JAN-1995; 95EP-0200023.
PR      11-JAN-1995; 95US-0371505.
PR      09-JUN-1995; 95EP-0201531.
PR      06-JUL-1995; 95US-0499092.
XX
PA      (COLL/) COLLEN D.
PA      (LEOV-) LEOVEN RES & DEV VZW.
XX
PI      Collen D;
XX
DR      WPI; 1996-333991/33.
XX
PT      New staphylokinase derivs. having reduced immunogenicity - useful
        for treating arterial thrombosis
XX
PS      Disclosure; Fig 1; 58pp; English.
XX
CC      Staphylokinase derivatives showing a reduced immunogenicity as
        compared to wild-type staphylokinase are claimed. The derivatives
        are useful as thrombolytic agents to treat arterial thrombosis and
        are pref. produced by eliminating at least one of the epitopes
        indicated in the features table. The epitopes are destroyed by
        replacing one or more amino acid residues in a charge cluster by an
        Ala residue. Mutations are introduced using site-directed
        mutagenesis on wild-type staphylokinase genomic DNA from the S.aureus
        lysogenic strain SakSTAR. The present sequence is that of wild-type
        SakSTAR staphylokinase.
XX
SQ      Sequence 136 AA;

Query Match      100.0%; Score 136; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.3e-131;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SSSFDKGYKKGDDASYFEPTGPYLMVNTGYVDSKGNELLSPHYVEFPKPGTTLTKETI 60
        |||
Db      1 sssfdkgykkgddasysfeptgpylmvntgyvdskgnellspkgttltketi 60
OY      61 EYVEMALDATATYKKEFRVVELDPSAKIEVYYDKNKKKEETKSPFITEKGFVVPDLSEHI 120
        |||
Db      61 eyvewaldatatykefrvveldpksakievtydknkkkeetksfptekgfvpdlsehi 120
OY      121 KNPGENLITKVVIEKK 136
        |||
Db      121 knpgfnliltkvievkk 136

RESULT 3
AAB99421
ID      AAB99421 standard; Protein; 136 AA.
XX
AC      AAB99421;
XX
DT      28-AUG-2001 (first entry)
XX
DE      Staphylokinase (SakSTAR) primary protein sequence.
XX
KW      Staphylokinase; Staphylococcus aureus; SakSTAR; T-cell epitope;
        immunogenic; thrombolytic; acute myocardial infarction; immunogenicity.
XX
OS      Staphylococcus aureus.
XX
PN      W0200140281-A2.
XX
PD      07-JUN-2001.
XX

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```

PF 01-DEC-2000; 2000WO-EP12229.
XX
XX 02-DEC-1999; 99EP-0204093.
XX
XX (THRO-) THROMB-X NV.
XX
XX Warmerdam PAM, Plaaisance SDNGH, Collen DJ, De Maeyer MCH;
XX
XX WPI: 2001-374786/39.
XX
XX Reducing immunogenicity of protein (P) by eliminating T cell epitopes
XX in test peptides having amino acid sequence corresponding to (P) and
XX modifying amino acid sequence of (P) according to test peptide
XX modifications -
XX
XX PS Disclosure; Fig 1: 50pp; English.
XX
XX The present invention describes a method for reducing the immunogenicity
XX of a peptide or protein (I), where (I) can be staphylokinase (SakSTAR)
XX isolated from Staphylococcus aureus. The method involves designing a
XX series of overlapping test peptides having an amino acid sequence
XX corresponding to (I), modifying test peptides which are identified to
XX comprise one or more T-cell epitopes, such that they are reduced or
XX eliminated, and repeating the T-cell eliminating modifications for (I)
XX to produce a modified peptide or protein. Methods for the present
XX invention can be used for the treatment, diagnosis or prophylaxis or
XX for the preparation of a pharmaceutical composition for the treatment,
XX diagnosis or prophylaxis of a human subject. Staphylokinase is used as a
XX potent thrombolytic agent in patients with acute myocardial infarction.
XX The method is useful for reducing cell based immunogenicity of non-human
XX proteins such as streptokinase or antibodies or their fragments, from
XX other species, for diagnostics and treatment of human disease. AAB99400
XX to AAB99449 represent amino acid sequences used in the exemplification
XX of the present invention.
XX
XX SQ Sequence 136 AA:
XX
XX Query Match 100.0%; Score 136; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 3.9e-131;
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSFSDGKTKKGGDASYFEPTGTYLMVNTGVDSKGNELSPHYVEPIKPGTTLRKEKI 60
XX |||||||
XX Db 1 sssfdkgkykkgdasyfepctgpylmvntgyvskgnellsplyvefpikpgttltkeki 60
XX
XX QY 61 EYVEWALDATAATKKEFRVVELDPSAKIEVYYVDKNNKKEETKSPITTEKGFVVPDLSEHI 120
XX |||||||
XX Db 61 eyvewaldataatkefrvveldpsakievtyydknnkkeetsfpitkgyfvvpdlsehi 120
XX
XX QY 121 KNGFNLITKRVYIEKK 136
XX |||||||
XX Db 121 knpgfnlilkvylekk 136
XX
XX RESULT 4
XX AAB61909
XX ID AAB61909 standard; Protein: 136 AA.
XX
XX AC AAB61909;
XX
XX DT 08-MAY-2001 (first entry)
XX
XX DE S. aureus staphylokinase G34S variant.
XX
XX XX Immunogenicity; staphylokinase; variant; stability.
XX
XX OS Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 34 /label= G34S
XX FT /note= "wild-type Gly is replaced by Ser"

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```

XX
XX WO200104287-A1.
XX
XX PN 18-JAN-2001.
XX
XX PD 06-JUL-2000; 2000WO-DK00371.
XX
XX PF 07-JUL-1999; 99DK-0000988.
XX
XX PR 27-AUG-1999; 99DK-0001196.
XX
XX PR 02-MAR-2000; 2000DK-0000339.
XX
XX PR 18-MAY-2000; 2000DK-0000804.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX PA Halkier T, Pedersen AH, Okkels JS;
XX
XX PI WPI: 2001-138342/14.
XX
XX DR
XX
XX XX Producing polypeptides with altered immunogenicity or improved
XX stability, comprises expressing a diversified nucleotide sequence
XX population and selecting polypeptides with altered immunogenicity or
XX improved stability -
XX
XX PS Example 1; Page 76; 83pp; English.
XX
XX The invention relates to a method of altering immunogenicity and/or
XX increasing stability of a polypeptide of interest. The method comprises
XX (a) expressing a diversified population of nucleotide sequences encoding
XX a polypeptide of interest; (b) screening the polypeptides expressed for
XX function, immunogenicity and/or stability; and (c) selecting functional
XX polypeptides with altered immunogenicity and/or increased stability. The
XX method is used to improve the properties of polypeptides, in particular
XX to alter the immunogenicity and/or increase the functional in vivo half-
XX life of the polypeptide. The method uses a high throughput system that
XX makes it possible to search several orders of magnitude more polypeptides
XX than is possible by previously known approaches. This enhances the chance
XX of finding the optimal variant from the many thousands of variants that
XX CC may be produced. The present sequence represents S. aureus staphylokinase
XX variant sequence, used to exemplify the method of the invention.
XX
XX SQ Sequence 136 AA:
XX
XX Query Match 100.0%; Score 136; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 3.9e-131;
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSFSDGKTKKGGDASYFEPTGTYLMVNTGVDSKGNELSPHYVEPIKPGTTLRKEKI 60
XX |||||||
XX Db 1 sssfdkgkykkgdasyfepctgpylmvntgyvskgnellsplyvefpikpgttltkeki 60
XX
XX QY 61 EYVEWALDATAATKKEFRVVELDPSAKIEVYYVDKNNKKEETKSPITTEKGFVVPDLSEHI 120
XX |||||||
XX Db 61 eyvewaldataatkefrvveldpsakievtyydknnkkeetsfpitkgyfvvpdlsehi 120
XX
XX QY 121 KNGFNLITKRVYIEKK 136
XX |||||||
XX Db 121 knpgfnlilkvylekk 136
XX
XX RESULT 5
XX AAR39150
XX ID AAR39150 standard; Protein: 137 AA.
XX
XX AC AAR39150;
XX
XX DT 03-DEC-1993 (first entry)
XX
XX DE Staphylokinase SAK-STAR.
XX
XX XX Signal sequence, plasminogen activator; thrombosis; staphylokinase;
XX KW SAK.
XX
XX

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OS Staphylococcus aureus strain 23.
XX
PN W09313209-A.
XX
PD 08-JUL-1993.
XX
PE 28-DEC-1992; 92WO-EP02989.
XX
PR 30-DEC-1991; 91DE-4143279.
PR 22-JUN-1992; 92DE-4220516.
PR 01-DEC-1992; 92DE-4240801.
XX
PA (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAPARATE.
XX
PI Albrecht S, Behnke D, Guehrs K, Hartmann M, Schloft B;
XX
DR WPI; 1993-227325/28.
DR N-PSDB; AAO44270.
XX
PT Staphylo-kinase (SAK) sequences lacking sequences for signal
PT peptide(s) - for prodn. of proteins used as plasminogen
PT activators in thrombosis treatment, and monoclonal antibodies
PT against SAK
XX
PS Claim 3; Fig 3; 99pp; German.
XX
CC DNA encoding SAK lacking the signal peptide, is expressed
CC intracellularly. This avoids the problem of fast degradation of the
CC polypeptides or destruction of the host when expressed into the
CC medium or into the periplasm respectively. High expression is
CC possible and the chemically induced overprodn. is easy to handle.
CC Also, the prods. are homogeneous.
CC SAK-polypeptide derivs. are plasminogen activators for the
CC treatment of thrombosis.
XX
SQ Sequence 137 AA:

Query Match 100.0%; Score 136; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.9e-131;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSSFDKGYKKGGDASYPEPTGPIYLMVNTGVDSKGNELLSPHYVEFPKPGTTLTKKXI 60
DB 2 SSSfdkgkykkgddasyfepptgpylmvntgvdskgnellspHYVEfpIkpgtlltKekI 61
OY 61 EYVEMALDATAYKERRVVELDPSAKIEVTYYDKNNKKKEETKSFPITTEKGFVVPDLSEHI 120
DB 62 EYVewaldataykefrvveldpsakievtyydknnkkeeetksfptekgfivvpdlsehi 121
OY 121 KNPGFNLITRKVI 136
DB 122 knpgfnlItkvIekK 137

RESULT 6
ID AAO03102 standard; protein; 136 AA.
XX
AC AAO03102;
XX
DT 19-FEB-1997 (first entry)
XX
DE Staphylokinase derivative M19 with altered charge cluster 19.
XX
KW Staphylokinase; mutant; mutein; variant; immunogenicity; decrease;
KW derivative; SAKSTAR; arterial thrombosis; thrombolytic agent.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 134..136

FT /label= altered_M19_cluster
FT /note= "wild-type cluster 19 sequence Glu-Lys-Lys
FT has been replaced by Ala-Ala-Ala to reduce
FT immunogenicity"
XX
PD W09621016-A2.
XX
PD 11-JUL-1996.
XX
PE 03-JAN-1996; 96WO-EP00081.
XX
PR 17-NOV-1995; 95JP-0299781.
PR 06-JAN-1995; 95EP-0200023.
PR 11-JAN-1995; 95US-0371505.
PR 09-JUN-1995; 95EP-0201531.
PR 06-JUL-1995; 95US-0499092.
XX
PA (COLL-) COLLEN D.
PA (LEUV-) LEUVEN RES & DEV VZW.
XX
PI Collen D;
XX
DR WPI; 1996-333991/33.
XX
PT New staphylokinase derivs. having reduced immunogenicity - useful
PT for treating arterial thrombosis
XX
PS Example 2; Page -: 58pp; English.
XX
CC Staphylokinase derivatives showing a reduced immunogenicity as
CC compared to wild-type staphylokinase are claimed. The derivatives
CC are useful as thrombolytic agents to treat arterial thrombosis and
CC are pref. produced by eliminating at least one of the epitopes
CC indicated in the features table. The epitopes are destroyed by
CC replacing one or more amino acid residues in a charge cluster by an
CC Ala residue. Mutations are introduced using site-directed
CC mutagenesis on wild-type staphylokinase genomic DNA from the S.aureus
CC lysogenic strain SAKSTAR. The present sequence is a specific
CC example of a staphylokinase derivative according to the invention;
CC the sequence does not appear in the specification but can be generated
CC from the wild-type staphylokinase sequence using the description given
CC in Table 1 of the disclosure.
XX
SQ Sequence 136 AA:

Query Match 97.8%; Score 133; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.5e-128;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSSFDKGYKKGGDASYPEPTGPIYLMVNTGVDSKGNELLSPHYVEFPKPGTTLTKKXI 60
DB 1 SSSfdkgkykkgddasyfepptgpylmvntgvdskgnellspHYVEfpIkpgtlltKekI 60
OY 61 EYVEMALDATAYKERRVVELDPSAKIEVTYYDKNNKKKEETKSFPITTEKGFVVPDLSEHI 120
DB 61 EYVewaldataykefrvveldpsakievtyydknnkkeeetksfptekgfivvpdlsehi 120
OY 121 KNPGFNLITRKVI 133
DB 122 knpgfnlItkvI 133

RESULT 7
ID AAO03085 standard; protein; 136 AA.
XX
AC AAO03085;
XX
DT 19-FEB-1997 (first entry)
XX
DE Staphylokinase derivative M19 with altered charge cluster 19.
XX

KW Staphylokinase; mutant; mutein; variant; immunogenicity: decrease;
 XX derivative; SakSTAR; arterial thrombosis; thrombolytic agent.
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Region 134..136
 FT /label= altered M19 cluster
 FT /note= "wild-type cluster 19 sequence Glu-Lys-Lys
 FT has been replaced by Ala-Ala-Ala to reduce
 FT immunogenicity"
 XX
 XX EP721982-A1.
 XX
 XX 17-JUL-1996.
 XX
 XX PD 06-JAN-1995; 95EP-0200023.
 XX
 XX PR 06-JAN-1995; 95EP-0200023.
 XX
 XX PA (COLL/) COLLEN D J.
 XX (LEUV-) LEUVEN RES & DEV VZW.
 XX
 XX PI Collen D;
 XX
 XX DR WPI: 1996-322832/33.
 XX
 XX PT New staphylokinase mutants with reduced immunogenicity - useful for
 XX treating arterial thrombosis
 XX
 XX PS Example 2; Page -: 21pp; English.
 XX
 CC Staphylokinase derivatives showing a reduced immunogenicity as
 CC compared to wild-type staphylokinase are claimed. The derivatives
 CC are useful as thrombolytic agents to treat arterial thrombosis and
 CC are pref. produced by eliminating at least one of the epitopes
 CC indicated in the features table. The epitopes are destroyed by an
 CC replacing one or more amino acid residues in a charge cluster by an
 CC Ala residue. Mutations are introduced using site-directed
 CC mutagenesis on wild-type staphylokinase genomic DNA from the S. aureus
 CC lysogenic strain SakSTAR. The present sequence is a specific
 CC example of a staphylokinase derivative according to the invention;
 CC the sequence does not appear in the specification but can be generated
 CC from the wild-type staphylokinase sequence using the description given
 CC in Table 1 of the disclosure.
 CC
 XX SQ Sequence 136 AA:
 SQ
 Query Match 97.8%; Score 133; DB 17; Length 136;
 Best Local Similarity 100.0%; Pred. No. 4,5e-128;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SSSFDKGRKKYKGGDASYFEPTGPLYLMVNTGVDSKGNELSPHYVEPIKPGTTLTKRKI 60
 DB 1 sssfdkgykkgddasyfeptgplylmvntgvskgnellsphlyvefpikpgtltlckeki 60
 OY 61 EYVEMALDATAKFERRVVELDPSAKIEVYYDKNKKKEETKSFPITTEKGFVVPDLSEHI 120
 DB 61 eyvewaldatakyketriveldpsakievtydknkkkeetksfptlekgyfvvpdlsehi 120
 OY 121 KNPGFNLTIRKVY 133
 DB 121 knpgfnltirkvyl 133
 RESULT 8
 ID AAY15024 standard; Protein: 136 AA.
 XX
 AC AAY15024;
 XX

DT 03-NOV-1999 (first entry)
 DE Staphylokinase variant SakSTAR (V132L).
 XX
 XX Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
 KW SakSTAR (V132L); anti-thrombotic; fibrinolytic; cardiant; veterinary;
 KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
 KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 132
 FT /note= "Wild type Val is substituted by Leu"
 XX
 XX PN W09940198-A2.
 XX
 XX PD 12-AUG-1999.
 XX
 XX PD 04-FEB-1999; 99WO-EP00748.
 XX
 XX PR 06-FEB-1998; 98EP-0200365.
 XX 04-FEB-1998; 98EP-0200323.
 XX
 XX PA (COLL/) COLLEN D J.
 XX (LEUV-) LEUVEN RES & DEV VZW.
 XX
 XX PI Collen DJ;
 XX
 XX DR WPI: 1999-508504/42.
 XX
 XX PT Staphylokinase derivatives with reduced immunogenicity, used for,
 XX e.g. treatment of arterial thrombosis
 XX
 XX PS Claim 7; Page -: 101pp; English.
 XX
 CC The present sequence is a specifically claimed Staphylokinase SakSTAR
 CC variant. This variant has one aminoacid that has been substituted
 CC by another aminoacid that reduces the reactivity with monoclonal
 CC antibodies and absorption of SakSTAR-specific antibodies from plasma
 CC of patients treated with staphylokinase. The derivatives can also be
 CC substituted with cysteine modified with PEG to maintain the specific
 CC activity and significantly reduce the plasma clearance. They have
 CC altered immunogenicity without markedly reducing the specific activity.
 CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
 CC potency in human plasma. The new staphylokinase derivatives are used
 CC for treatment of arterial thrombosis, especially myocardial infarction.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the Staphylococcus aureus wild type staphylokinase sequence
 CC given in figure 1.
 CC
 XX SQ Sequence 136 AA:
 SQ
 Query Match 96.3%; Score 131; DB 20; Length 136;
 Best Local Similarity 100.0%; Pred. No. 5e-126;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SSSFDKGRKKYKGGDASYFEPTGPLYLMVNTGVDSKGNELSPHYVEPIKPGTTLTKRKI 60
 DB 1 sssfdkgykkgddasyfeptgplylmvntgvskgnellsphlyvefpikpgtltlckeki 60
 OY 61 EYVEMALDATAKFERRVVELDPSAKIEVYYDKNKKKEETKSFPITTEKGFVVPDLSEHI 120
 DB 61 eyvewaldatakyketriveldpsakievtydknkkkeetksfptlekgyfvvpdlsehi 120
 OY 121 KNPGFNLTIRKVY 131
 DB 121 knpgfnltirkvyl 131

```

RESULT 9
AA15025
ID AAY15025 standard; Protein: 136 AA.
XX
XX
AC AAY15025;
XX
XX
DT 03-NOV-1999 (first entry)
XX
XX
DE Staphylokinase variant SakSTAR (V132P).
XX
XX
KW Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KW SakSTAR (V132P); anti-thrombotic; fibrinolytic; cardiant; veterinary;
KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 132 /note="Wild type Val is substituted by Thr"
FT
XX
XX
PN MO9940198-A2.
XX
XX
PD 12-AUG-1999.
XX
XX
PE 04-FEB-1999; 99WO-EP00748.
XX
XX
PR 06-FEB-1998; 98EP-0200365.
PR 04-FEB-1998; 98EP-0200323.
XX
XX
PA (COLL/) COLLEN D J.
PA (LEUV-) LEUVEN RES & DEV VZW.
XX
XX
PI Collen DJ;
XX
XX
DR WPI: 1999-508504/42.
XX
XX
PT Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis
XX
XX
PS Claim 7; Page -: 101pp; English.
XX
XX
CC The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteinen modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in figure 1.
XX
XX
SQ Sequence 136 AA;

```

Query Match 96.3%; Score 131; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 5e-126;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SSSPFGKGYKKGGDDASYEPPTGPIYLAWNTGVDSKGNELSHYVEFPKPKPTITLTKKI 60
    |||||||
DB 1 sssitkgkykgyddasyfepitgpylmvntgvdsksynelshpyvefpikpkitltkkl 60
OY 61 EYVVEALDATATYKRFRRVLELDPSSAKIEVYTDKNKKKETSPFTEKGFFVVPDLSEHI 120
    |||||||
DB 61 eyvewaldatakykefrvleldpsakievtytdknkkkeetksfpitkgffvvpdlsehi 120

```

```

OY 121 KNGFNLITKV 131
    |||||||
DB 121 knpfnliltkv 131

RESULT 10
AA15026
ID AAY15026 standard; Protein: 136 AA.
XX
XX
AC AAY15026;
XX
XX
DT 03-NOV-1999 (first entry)
XX
XX
DE Staphylokinase variant SakSTAR (V132N).
XX
XX
KW Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KW SakSTAR (V132N); anti-thrombotic; fibrinolytic; cardiant; veterinary;
KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 132 /note="Wild type Val is substituted by Asn"
FT
XX
XX
PN MO9940198-A2.
XX
XX
PD 12-AUG-1999.
XX
XX
PE 04-FEB-1999; 99WO-EP00748.
XX
XX
PR 06-FEB-1998; 98EP-0200365.
PR 04-FEB-1998; 98EP-0200323.
XX
XX
PA (COLL/) COLLEN D J.
PA (LEUV-) LEUVEN RES & DEV VZW.
XX
XX
PI Collen DJ;
XX
XX
DR WPI: 1999-508504/42.
XX
XX
PT Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis
XX
XX
PS Claim 7; Page -: 101pp; English.
XX
XX
CC The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteine modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in figure 1.
XX
XX
SQ Sequence 136 AA;

```

Query Match 96.3%; Score 131; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 5e-126;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SSSPFGKGYKKGGDDASYEPPTGPIYLAWNTGVDSKGNELSHYVEFPKPKPTITLTKKI 60

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Db      1 sssfdkgykkggdasyfeptgpylmvntgvdskgnellsphvvefpikpgtltlckek1 60
QY      61 EYVEMALDAtAKKEFRVVLDPsAKIEVYYRNKKKKKEETKSPITTEKGFVVPDSEH1 120
Db      61 eyvewaldataykeftrvveldpssaklevtydknkkkeetskfpittekgtfvvpdlseh1 120
QY      121 KNEGFNLITKV 131
Db      121 knpgfnliltkv 131

```

RESULT 11

AA15027
ID AAY15027 standard; Protein; 136 AA.

AC AAY15027;

DT 03-NOV-1999 (first entry)

DE Staphylokinase variant SakSTAR (V132R).

XX Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KM SakSTAR (V132R); anti-thrombotic; fibrinolytic; cardiant; veterinary;

XX Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KM monoclonal antibody; polyethylene glycol; PEG; plasma clearance.

XX Staphylococcus aureus.
OS Synthetic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 132 /note= "Wild type Val is substituted by Arg"

PN WO9940198-A2.

PD 12-AUG-1999.

PF 04-FEB-1999; 99WO-EP00748.

PR 06-FEB-1998; 98EP-0200365.

PR 04-FEB-1998; 98EP-0200323.

XX (COLL/) COLLEN D J.

PA (LEUV-) LEUVEN RES & DEV VZW.

PI Collen DJ;

DR WPI: 1999-508504/42.

XX Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis

XX Claim 7; Page -: 101pp; English.

XX The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteine modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in Figure 1.

XX Sequence 136 AA;

```

Query Match          96.3%; Score 131; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. Se-126;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 SSSFDKGRYKGGDASyfeptgpylmvntgvdskgnellsphvvefpikpgtltlckek1 60
Db      1 sssfdkgykkggdasyfeptgpylmvntgvdskgnellsphvvefpikpgtltlckek1 60
QY      61 EYVEMALDAtAKKEFRVVLDPsAKIEVYYRNKKKKKEETKSPITTEKGFVVPDSEH1 120
Db      61 eyvewaldataykeftrvveldpssaklevtydknkkkeetskfpittekgtfvvpdlseh1 120
QY      121 KNEGFNLITKV 131
Db      121 knpgfnliltkv 131

```

RESULT 12

AA15016
ID AAY15016 standard; Protein; 136 AA.

AC AAY15016;

DT 03-NOV-1999 (first entry)

DE Staphylokinase variant SakSTAR (V132A).

XX Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KM SakSTAR (V132A); anti-thrombotic; fibrinolytic; cardiant; veterinary;

XX Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KM monoclonal antibody; polyethylene glycol; PEG; plasma clearance.

XX Staphylococcus aureus.
OS Synthetic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 132 /note= "Wild type Val is substituted by Ala"

PN WO9940198-A2.

PD 12-AUG-1999.

PF 04-FEB-1999; 99WO-EP00748.

PR 06-FEB-1998; 98EP-0200365.

PR 04-FEB-1998; 98EP-0200323.

XX (COLL/) COLLEN D J.

PA (LEUV-) LEUVEN RES & DEV VZW.

PI Collen DJ;

DR WPI: 1999-508504/42.

XX Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis

XX Claim 7; Page -: 101pp; English.

XX The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteine modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.

CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in figure 1.

CC Sequence 136 AA;

Query Match 96.3%; Score 131; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 5e-126;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSPFGKYYKGGDASYPEPTGPIYLVWVTGVDKGNELSPHYVEPIKPGTTLTKRKI 60
DB 1 sssstkgkyykgyddasypfcgpylmvntvgvdskgnellspkyvefpikpgtltkxki 60
OY 61 EYYEWALDATALYKKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITKGFVVPDLSEHI 120
DB 61 eyyewaldatalykefrvveldpesakievtydknkkkeetksfptkgyfvvpdlsehi 120
OY 121 KNPGFNLTIKV 131
DB 121 knpgfnliltkv 131

RESULT 13

AAW03087
ID AAW03087 standard; protein; 136 AA.

AAW03087;

19-FEB-1997 (first entry)

Staphylokinase derivative M20 with altered charge cluster 20.

Staphylokinase; mutant; mutein; variant; immunogenicity: decrease;
derivative; SakSTAR; arterial thrombosis; thrombolytic agent.

Staphylococcus aureus.
Synthetic.

Key 5.6 Location/Qualifiers
Region /label= altered_M20_cluster
/note= "wild type cluster 20 sequence Asp-Lys
has been replaced by Ala-Ala to
reduce immunogenicity"

W09621016-A2.

11-JUL-1996.

03-JAN-1996; 96WO-EP00081.

17-NOV-1995; 95JP-0299781.

06-JAN-1995; 95EP-0200023.

11-JAN-1995; 95US-0371505.

09-JUN-1995; 95EP-0201531.

06-JUL-1995; 95US-0499092.

(COLL/) COLLEN D.

(LEUV-) LEUVEN RES & DEV VZW.

Colleen D;

WPI; 1996-333991/33.

New staphylokinase derivs. having reduced immunogenicity - useful
for treating arterial thrombosis
Example 2; Page -: 58pp; English.
Staphylokinase derivatives showing a reduced immunogenicity as
compared to wild-type staphylokinase are claimed. The derivatives

CC are useful as thrombolytic agents to treat arterial thrombosis and
CC are pref. produced by eliminating at least one of the epitopes
CC indicated in the features table. The epitopes are destroyed by
CC replacing one or more amino acid residues in a charge cluster by an
CC Ala residue. Mutations are introduced using site-directed
CC mutagenesis on wild-type staphylokinase genomic DNA from the S. aureus
CC lysogenic strain SakSTAR. The present sequence is a specific
CC example of a staphylokinase derivative according to the invention;
CC the sequence does not appear in the specification but can be generated
CC from the wild-type staphylokinase sequence using the description given
CC in Table 1 of the disclosure.

CC Sequence 136 AA;

Query Match 95.6%; Score 130; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 5.2e-125;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GKYYKGGDASYPEPTGPIYLVWVTGVDKGNELSPHYVEPIKPGTTLTKRKIYYEW 66
DB 7 gkyykgyddasypfcgpylmvntvgvdskgnellspkyvefpikpgtltkxkleyyew 66
OY 67 ALDATALYKKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITKGFVVPDLSEHIKPGFN 126
DB 67 aldataalykefrvveldpesakievtydknkkkeetksfptkgyfvvpdlsehi kpgfn 126
OY 127 LITKVVIERK 136
DB 127 litkvvlekk 136

RESULT 14

AAW03101
ID AAW03101 standard; protein; 136 AA.

AAW03101;

19-FEB-1997 (first entry)

Staphylokinase derivative M18 with altered charge cluster 18.

Staphylokinase; mutant; mutein; variant; immunogenicity: decrease;
derivative; SakSTAR; arterial thrombosis; thrombolytic agent.

Staphylococcus aureus.
Synthetic.

Key 130 Location/Qualifiers
Region /label= altered_M18_cluster
/note= "wild type cluster 18 sequence Lys
has been replaced by Ala to reduce
immunogenicity"

W09621016-A2.

11-JUL-1996.

03-JAN-1996; 96WO-EP00081.

17-NOV-1995; 95JP-0299781.

06-JAN-1995; 95EP-0200023.

11-JAN-1995; 95US-0371505.

09-JUN-1995; 95EP-0201531.

06-JUL-1995; 95US-0499092.

(COLL/) COLLEN D.

(LEUV-) LEUVEN RES & DEV VZW.

Colleen D;

WPI; 1996-333991/33.

```

XX New staphylokinase derivs. having reduced immunogenicity - useful
PT for treating arterial thrombosis
PS
XX Example 2: Page -: 58pp; English.
XX
CC Staphylokinase derivatives showing a reduced immunogenicity as
CC compared to wild-type staphylokinase are claimed. The derivatives
CC are useful as thrombolytic agents to treat arterial thrombosis and
CC are pref. produced by eliminating at least one of the epitopes
CC indicated in the features table. The epitopes are destroyed by
CC replacing one or more amino acid residues in a charge cluster by an
CC Ala residue. Mutations are introduced using site-directed
CC mutagenesis on wild-type staphylokinase genomic DNA from the S.aureus
CC lysogenic strain SakSTAR. The present sequence is a specific
CC example of a staphylokinase derivative according to the invention;
CC the sequence does not appear in the specification but can be generated
CC from the wild-type staphylokinase sequence using the description given
CC in Table 1 of the disclosure.
XX
SQ Sequence 136 AA:

Query Match          94.9% Score 129; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 5.Se-124;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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Db 1 sssfdkgykkggddasyleptgpylmvntvgdsksgnellsphyvefpikpgtltlkeki 60

QY 61 EYYEWALDATALAKCFRRVELLDPSAKIEVTYYDKNKKKEETKSPTTEKGVPVPLSEHI 120
Db 61 eyyewaldatalakefrvelldpsakievttydknkkkeetksfptekegvvpplsehi 120

QY 121 KNPGFNLT 129
Db 121 knpgfnlilt 129

RESULT 15
AAAY15023
ID AAY15023 standard; Protein: 136 AA.
XX
AC AAY15023;
XX
DT 03-NOV-1999 (first entry)
XX
DE Staphylokinase variant SakSTAR (KL30T).
XX
KW Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KW SakSTAR (KL30T); anti-thrombotic; fibrinolytic; cardiant; veterinary;
KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 130 /note= "Wild type Lys is substituted by Thr"
PN WC09A40198-A2.
XX
PD 12-AUG-1999.
XX
PE 04-FEB-1999; 99MO-EP00748.
XX
PR 06-FEB-1998; 98EP-0200365.
PR 04-FEB-1998; 98EP-0200323.
XX
COLL/ COLLEEN D J.
LEU/- LEUVEN RES & DEV VZW.

```

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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:43:45 ; Search time 12.66 Seconds

(without alignments)
241.742 Million cell updates/sec

Title: US-09-601-490-1

Perfect score: 136

Sequence: 1 SSSFDKXGKXKGGDASYPEP.....SEHIKNPGLITKVIIEKK 136

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/laa/5A.COMB.pep.*
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3: /cgn2_6/ptodata/2/laa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/laa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/laa/PCITUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	136	1 US-08-371-505-2	Sequence 2, Appli
2	136	100.0	136	2 US-08-784-971-5	Sequence 5, Appli
3	136	100.0	137	1 US-08-256-261-6	Sequence 6, Appli
4	136	100.0	137	3 US-08-852-289-6	Sequence 6, Appli
5	102	75.0	137	1 US-08-256-261-4	Sequence 4, Appli
6	102	75.0	137	3 US-08-852-299-4	Sequence 4, Appli
7	93	68.4	123	1 US-08-256-261-10	Sequence 10, Appli
8	93	68.4	123	3 US-08-852-299-10	Sequence 10, Appli
9	93	68.4	127	1 US-08-256-261-8	Sequence 8, Appli
10	93	68.4	127	3 US-08-852-299-8	Sequence 8, Appli
11	93	68.4	137	1 US-08-256-261-2	Sequence 2, Appli
12	93	68.4	137	1 US-08-256-261-12	Sequence 12, Appli
13	93	68.4	137	1 US-08-256-261-14	Sequence 14, Appli
14	93	68.4	137	3 US-08-852-299-2	Sequence 2, Appli
15	93	68.4	137	3 US-08-852-289-12	Sequence 12, Appli
16	93	68.4	137	3 US-08-852-299-14	Sequence 14, Appli
17	93	68.4	163	1 US-08-256-261-17	Sequence 17, Appli
18	93	68.4	163	3 US-08-852-299-17	Sequence 17, Appli
19	82	60.3	126	1 US-08-075-545-2	Sequence 2, Appli
20	82	60.3	163	1 US-08-075-545-1	Sequence 1, Appli
21	82	60.3	163	1 US-08-934-222-21	Sequence 21, Appli
22	82	60.3	163	1 US-08-934-222-22	Sequence 22, Appli
23	82	60.3	163	1 US-08-934-402-21	Sequence 21, Appli
24	82	60.3	163	1 US-08-934-402-22	Sequence 22, Appli
25	82	60.3	163	1 US-09-207-621-21	Sequence 21, Appli
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27	82	60.3	163	1 US-08-532-818-21	Sequence 21, Appli

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30	12	8.8	12	3 US-09-231-797-22	Sequence 22, Appli
31	12	8.8	12	3 US-08-934-224-21	Sequence 21, Appli
32	12	8.8	12	3 US-08-934-224-22	Sequence 22, Appli
33	12	8.8	12	3 US-08-934-843-21	Sequence 21, Appli
34	12	8.8	12	3 US-08-934-843-22	Sequence 22, Appli
35	12	8.8	12	4 US-08-934-223-21	Sequence 21, Appli
36	12	8.8	12	4 US-08-934-223-22	Sequence 22, Appli
37	12	8.8	12	4 US-09-413-492-21	Sequence 21, Appli
38	12	8.8	12	4 US-09-413-492-22	Sequence 22, Appli
39	12	8.8	12	4 US-08-934-222-23	Sequence 23, Appli
40	12	8.8	12	4 US-08-934-402-23	Sequence 23, Appli
41	12	8.8	12	4 US-09-207-621-23	Sequence 23, Appli
42	12	8.8	12	2 US-08-532-818-23	Sequence 23, Appli
43	12	8.8	12	3 US-09-231-797-23	Sequence 23, Appli
44	12	8.8	12	3 US-08-934-224-23	Sequence 23, Appli
45	12	8.8	12	3 US-08-934-843-23	Sequence 23, Appli
46	12	8.8	12	4 US-08-934-223-23	Sequence 23, Appli
47	12	8.8	12	4 US-09-413-492-23	Sequence 23, Appli
48	9	6.6	12	2 US-08-934-222-20	Sequence 20, Appli
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51	9	6.6	12	2 US-08-532-818-20	Sequence 20, Appli
52	9	6.6	12	3 US-09-231-797-20	Sequence 20, Appli
53	9	6.6	12	3 US-08-934-224-20	Sequence 20, Appli
54	9	6.6	12	3 US-08-934-843-20	Sequence 20, Appli
55	9	6.6	12	4 US-08-934-223-20	Sequence 20, Appli
56	9	6.6	12	4 US-09-413-492-20	Sequence 20, Appli
57	7	5.1	7	4 US-08-657-339A-9	Sequence 9, Appli
58	7	5.1	7	4 US-09-588-256-4	Sequence 4, Appli
59	7	5.1	7	2 US-08-659-251-5	Sequence 5, Appli
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61	6	5.1	7	5 PCT-US96-11445-5	Sequence 5, Appli
62	6	4.4	22	4 US-09-177-249-302	Sequence 302, Appli
63	6	4.4	139	1 US-08-120-607A-11	Sequence 11, Appli
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65	6	4.4	220	4 US-08-297-431B-31	Sequence 31, Appli
66	6	4.4	221	4 US-08-297-431B-2	Sequence 2, Appli
67	6	4.4	221	4 US-08-297-431B-16	Sequence 16, Appli
68	6	4.4	221	4 US-08-297-431B-6	Sequence 6, Appli
69	6	4.4	221	4 US-08-297-431B-8	Sequence 8, Appli
70	6	4.4	221	4 US-08-297-431B-10	Sequence 10, Appli
71	6	4.4	221	4 US-08-297-431B-12	Sequence 12, Appli
72	6	4.4	221	4 US-08-297-431B-14	Sequence 14, Appli
73	6	4.4	221	4 US-08-297-431B-18	Sequence 18, Appli
74	6	4.4	221	4 US-08-297-431B-20	Sequence 20, Appli
75	6	4.4	228	4 US-09-303-064-24	Sequence 24, Appli
76	6	4.4	230	4 US-09-230-196-18	Sequence 18, Appli
77	6	4.4	230	4 US-09-230-196-23	Sequence 23, Appli
78	6	4.4	235	4 US-09-101-135-2	Sequence 2, Appli
79	6	4.4	235	4 US-09-303-064-27	Sequence 27, Appli
80	6	4.4	236	4 US-08-872-961A-4	Sequence 4, Appli
81	6	4.4	271	2 US-09-231-258-4	Sequence 4, Appli
82	6	4.4	272	3 US-09-101-135-8	Sequence 8, Appli
83	6	4.4	338	3 US-07-954-840A-8	Sequence 8, Appli
84	6	4.4	345	1 US-07-954-840A-16	Sequence 16, Appli
85	6	4.4	345	1 US-07-954-840A-18	Sequence 18, Appli
86	6	4.4	345	1 US-07-954-840A-20	Sequence 20, Appli
87	6	4.4	345	1 US-07-954-840A-22	Sequence 22, Appli
88	6	4.4	345	1 US-07-954-840A-24	Sequence 24, Appli
89	6	4.4	345	1 US-07-954-840A-26	Sequence 26, Appli
90	6	4.4	345	1 US-07-954-840A-31	Sequence 31, Appli
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92	6	4.4	347	1 US-07-954-840A-6	Sequence 6, Appli
93	6	4.4	347	1 US-07-954-840A-28	Sequence 28, Appli
94	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
95	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
96	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
97	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
98	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
99	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli
100	6	4.4	347	1 US-07-954-840A-29	Sequence 29, Appli

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102	6	4.4	398	1	US-08-442-043A-2	Sequence 2, Appl	175	6	4.4	761	3	US-09-012-710-13	Sequence 13, Appl
103	6	4.4	398	5	PCT-US91-03478-2	Sequence 2, Appl	176	6	4.4	761	3	US-09-625-188-14	Sequence 14, Appl
104	6	4.4	415	5	PCT-US93-00601-2	Sequence 2, Appl	177	6	4.4	797	1	US-08-453-695A-112	Sequence 11, App
105	6	4.4	415	5	PCT-US94-07107A-2	Sequence 2, Appl	178	6	4.4	797	1	US-08-268-161A-112	Sequence 112, App
106	6	4.4	420	3	US-08-665-871-58	Sequence 58, Appl	179	6	4.4	797	2	US-08-453-702A-112	Sequence 112, App
107	6	4.4	426	5	PCT-US94-07107A-7	Sequence 7, Appl	180	6	4.4	797	5	US-09-099-639-112	Sequence 112, App
108	6	4.4	443	1	US-07-940-245-2	Sequence 2, Appl	181	6	4.4	797	5	PCT-US95-08071-112	Sequence 112, App
109	6	4.4	443	1	US-08-226-486-2	Sequence 2, Appl	182	6	4.4	803	1	US-08-062-368-2	Sequence 11, App
110	6	4.4	445	4	US-08-083-945C-2	Sequence 2, Appl	183	6	4.4	803	4	US-09-118-442-2	Sequence 2, Appl
111	6	4.4	445	4	US-08-083-945C-7	Sequence 2, Appl	184	6	4.4	803	4	US-09-677-064-2	Sequence 2, Appl
112	6	4.4	489	1	US-08-124-674-2	Sequence 7, Appl	185	6	4.4	814	1	US-08-233-788A-42	Sequence 42, Appl
113	6	4.4	489	1	US-08-589-893-2	Sequence 2, Appl	186	6	4.4	834	2	US-08-677-734A-9	Sequence 9, Appl
114	6	4.4	489	1	US-08-589-893-4	Sequence 6, Appl	187	6	4.4	834	2	US-08-677-734A-10	Sequence 10, Appl
115	6	4.4	489	1	US-08-589-893-6	Sequence 8, Appl	188	6	4.4	966	2	US-08-868-786-2	Sequence 2, Appl
116	6	4.4	489	1	US-08-589-893-8	Sequence 10, Appl	189	6	4.4	1003	3	US-08-851-843A-217	Sequence 217, App
117	6	4.4	489	1	US-08-589-893-10	Sequence 12, Appl	190	6	4.4	1003	4	US-08-974-549A-336	Sequence 336, App
118	6	4.4	489	1	US-08-589-893-12	Sequence 14, Appl	191	6	4.4	1003	4	US-08-974-549A-217	Sequence 217, App
119	6	4.4	489	1	US-08-589-893-14	Sequence 16, Appl	192	6	4.4	1132	3	US-08-851-843A-225	Sequence 225, App
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121	6	4.4	489	1	US-08-589-893-18	Sequence 20, Appl	194	6	4.4	1132	4	US-08-974-549A-344	Sequence 344, App
122	6	4.4	489	1	US-08-589-893-20	Sequence 22, Appl	195	6	4.4	1132	4	US-08-854-050-225	Sequence 225, App
123	6	4.4	489	1	US-08-589-893-22	Sequence 24, Appl	196	6	4.4	1134	4	US-08-974-549A-611	Sequence 611, App
124	6	4.4	489	1	US-08-589-893-24	Sequence 26, Appl	197	6	4.4	1189	4	US-08-974-549A-613	Sequence 613, App
125	6	4.4	489	1	US-08-589-893-26	Sequence 28, Appl	198	6	4.4	1200	4	US-08-974-549A-612	Sequence 612, App
126	6	4.4	489	2	US-09-020-991-2	Sequence 4, Appl	199	6	4.4	1244	3	US-08-938-291A-5	Sequence 5, Appl
127	6	4.4	489	2	US-09-020-991-4	Sequence 6, Appl	200	6	4.4	1285	4	US-08-974-549A-600	Sequence 600, App
128	6	4.4	489	2	US-09-020-991-6	Sequence 8, Appl	201	6	4.4	1354	3	US-08-685-871-2	Sequence 2, Appl
129	6	4.4	489	2	US-09-020-991-8	Sequence 10, Appl	202	6	4.4	1407	4	US-08-974-549A-628	Sequence 628, App
130	6	4.4	489	2	US-09-020-991-10	Sequence 12, Appl	203	6	4.4	1407	4	US-08-843-417-2	Sequence 2, Appl
131	6	4.4	489	2	US-09-020-991-12	Sequence 14, Appl	204	6	4.4	1956	4	US-08-843-417-2	Sequence 2, Appl
132	6	4.4	489	2	US-09-020-991-14	Sequence 16, Appl	205	6	4.4	2618	5	PCT-US94-00198-4	Sequence 28, Appl
133	6	4.4	489	2	US-09-020-991-16	Sequence 18, Appl	206	6	4.4	3079	4	US-09-428-517-4	Sequence 4, Appl
134	6	4.4	489	2	US-09-020-991-18	Sequence 20, Appl	207	6	4.4	3519	4	US-09-428-517-2	Sequence 4, Appl
135	6	4.4	489	2	US-09-020-991-20	Sequence 22, Appl	208	5	3.7	4150	5	US-08-371-505-1	Sequence 1, Appl
136	6	4.4	489	2	US-09-020-991-22	Sequence 24, Appl	209	5	3.7	6	1	US-08-014-979-93	Sequence 83, Appl
137	6	4.4	489	2	US-09-062-890-4	Sequence 2, Appl	210	5	3.7	7	4	US-08-657-339A-3	Sequence 3, Appl
138	6	4.4	489	2	US-09-062-890-6	Sequence 4, Appl	211	5	3.7	9	2	US-08-350-260A-523	Sequence 523, App
139	6	4.4	489	2	US-09-062-890-8	Sequence 6, Appl	212	5	3.7	10	6	5190919-39	Patent No. 5190919
140	6	4.4	489	2	US-09-062-890-10	Sequence 8, Appl	213	5	3.7	11	1	US-07-946-421-22	Sequence 22, Appl
141	6	4.4	489	2	US-09-062-890-12	Sequence 10, Appl	214	5	3.7	11	1	US-08-471-780C-122	Sequence 122, App
142	6	4.4	489	2	US-09-062-890-14	Sequence 12, Appl	215	5	3.7	11	1	US-08-467-882B-122	Sequence 122, App
143	6	4.4	489	2	US-09-062-890-16	Sequence 14, Appl	216	5	3.7	11	1	US-08-471-882A-122	Sequence 122, App
144	6	4.4	489	2	US-09-062-890-18	Sequence 16, Appl	217	5	3.7	11	2	US-08-466-710C-122	Sequence 122, App
145	6	4.4	489	2	US-09-062-890-20	Sequence 18, Appl	218	5	3.7	11	3	US-08-468-739C-122	Sequence 122, App
146	6	4.4	489	2	US-09-062-890-22	Sequence 20, Appl	219	5	3.7	11	3	US-08-649-100-24	Sequence 122, App
147	6	4.4	489	2	US-09-062-890-24	Sequence 22, Appl	220	5	3.7	11	4	US-08-569-147-61	Sequence 61, Appl
148	6	4.4	489	2	US-09-062-890-26	Sequence 24, Appl	221	5	3.7	11	6	5190919-38	Patent No. 5190919
149	6	4.4	489	2	US-09-062-890-28	Sequence 26, Appl	222	5	3.7	11	6	5190919-40	Patent No. 5190919
150	6	4.4	489	2	US-09-062-890-30	Sequence 28, Appl	223	5	3.7	12	2	US-08-934-422-132	Sequence 132, App
151	6	4.4	489	2	US-09-062-890-32	Sequence 30, Appl	224	5	3.7	12	2	US-08-933-402-132	Sequence 132, App
152	6	4.4	489	2	US-09-062-890-34	Sequence 32, Appl	225	5	3.7	12	2	US-09-207-621-132	Sequence 132, App
153	6	4.4	489	2	US-09-062-890-36	Sequence 34, Appl	226	5	3.7	12	2	US-08-532-818-132	Sequence 132, App
154	6	4.4	489	2	US-09-062-890-38	Sequence 36, Appl	227	5	3.7	12	3	US-09-231-797-132	Sequence 132, App
155	6	4.4	489	2	US-09-062-890-40	Sequence 38, Appl	228	5	3.7	12	3	US-08-934-224-132	Sequence 132, App
156	6	4.4	506	3	US-08-888-998-2	Sequence 2, Appl	229	5	3.7	12	3	US-08-933-843-132	Sequence 132, App
157	6	4.4	506	4	US-09-362-633-2	Sequence 32, Appl	230	5	3.7	12	4	US-08-934-223-132	Sequence 132, App
158	6	4.4	506	4	US-09-303-064-52	Sequence 602, App	231	5	3.7	13	6	5190919-7	Patent No. 5190919
159	6	4.4	538	2	US-08-974-549A-602	Sequence 11, Appl	232	5	3.7	13	6	5190919-32	Patent No. 5190919
160	6	4.4	585	4	US-08-453-848-11	Sequence 11, Appl	233	5	3.7	15	2	US-08-659-567-23	Sequence 23, Appl
161	6	4.4	585	4	US-09-169-027-11	Sequence 19, Appl	234	5	3.7	16	1	US-08-218-025A-12	Sequence 12, Appl
162	6	4.4	585	2	US-08-453-848-19	Sequence 19, Appl	235	5	3.7	17	3	US-08-300-928C-24	Sequence 24, Appl
163	6	4.4	589	2	US-09-169-027-19	Sequence 19, Appl	236	5	3.7	17	3	US-08-430-944D-24	Sequence 24, Appl
164	6	4.4	589	2	US-08-453-848-13	Sequence 13, Appl	237	5	3.7	17	3	US-08-430-944D-24	Sequence 24, Appl
165	6	4.4	589	2	US-09-169-027-13	Sequence 13, Appl	238	5	3.7	17	3	US-08-431-184A-24	Sequence 24, Appl
166	6	4.4	592	4	US-08-453-848-17	Sequence 17, Appl	239	5	3.7	18	3	US-09-082-737-8	Sequence 8, Appl
167	6	4.4	592	4	US-09-370-807-12	Sequence 12, Appl	240	5	3.7	18	3	US-08-300-928C-25	Sequence 25, Appl
168	6	4.4	594	4	US-08-484-993B-10	Sequence 10, Appl	241	5	3.7	18	3	US-08-430-944D-25	Sequence 25, Appl
169	6	4.4	715	2	US-08-484-158B-10	Sequence 10, Appl	242	5	3.7	18	3	US-08-430-944D-25	Sequence 25, Appl
170	6	4.4	715	2	US-08-484-158B-10	Sequence 10, Appl	243	5	3.7	18	3	US-08-431-184A-25	Sequence 25, Appl
171	6	4.4	715	2	US-08-480-150A-10	Sequence 10, Appl	244	5	3.7	18	4	US-08-974-549A-163	Sequence 163, App
172	6	4.4	715	2	US-08-480-150A-10	Sequence 10, Appl	245	5	3.7	18	4	PCT-US91-02942-57	Sequence 57, App
173	6	4.4	715	3	US-08-458-731-10	Sequence 10, Appl	246	5	3.7	18	5		

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248	5	3.7	19	2	US-08-876-781-6	Sequence 6, Appli	321	5	3.7	33	4	US-08-836-252A-1	Sequence 1, Appli
249	5	3.7	21	1	US-07-807-529A-17	Sequence 17, Appli	322	5	3.7	33	4	US-09-082-279B-1105	Sequence 1105, Ap
250	5	3.7	21	3	US-08-300-928C-66	Sequence 66, Appli	323	5	3.7	33	4	US-09-082-279B-1106	Sequence 1106, Ap
251	5	3.7	21	3	US-08-430-944D-66	Sequence 66, Appli	324	5	3.7	34	4	US-09-082-279B-1107	Sequence 1107, Ap
252	5	3.7	21	3	US-08-430-014-66	Sequence 66, Appli	325	5	3.7	35	4	US-09-082-279B-1100	Sequence 1100, Ap
253	5	3.7	22	1	US-08-431-184-66	Sequence 66, Appli	326	5	3.7	35	4	US-09-082-279B-1102	Sequence 1102, Ap
254	5	3.7	22	1	US-08-343-943-7	Sequence 7, Appli	327	5	3.7	35	4	US-09-082-279B-1115	Sequence 1115, Ap
255	5	3.7	22	3	US-08-940-095-9	Sequence 9, Appli	328	5	3.7	35	4	US-09-082-279B-1158	Sequence 1158, Ap
256	5	3.7	22	3	US-08-940-093-9	Sequence 9, Appli	329	5	3.7	35	4	US-09-082-279B-1176	Sequence 1176, Ap
257	5	3.7	22	3	US-08-940-096-9	Sequence 9, Appli	330	5	3.7	35	4	US-09-082-279B-1185	Sequence 1185, Ap
258	5	3.7	22	4	US-09-082-279B-1292	Sequence 1292, Ap	331	5	3.7	35	4	US-09-082-279B-1166	Sequence 1166, Ap
259	5	3.7	22	4	US-09-082-279B-1327	Sequence 1327, Ap	332	5	3.7	35	4	US-09-082-279B-1311	Sequence 1311, Ap
260	5	3.7	22	4	US-09-465-719-9	Sequence 9, Appli	333	5	3.7	35	6	5190919-5	Patent No. 5190919
261	5	3.7	23	2	US-08-637-759B-242	Sequence 242, App	334	5	3.7	35	6	5190919-6	Patent No. 5190919
262	5	3.7	23	3	US-08-871-355A-242	Sequence 242, App	335	5	3.7	36	4	US-09-082-279B-1072	Sequence 1072, Ap
263	5	3.7	23	3	US-09-082-279B-1206	Sequence 1206, Ap	336	5	3.7	36	4	US-09-082-279B-1073	Sequence 1073, Ap
264	5	3.7	23	4	US-09-082-279B-1207	Sequence 1207, Ap	337	5	3.7	36	6	5190919-15	Patent No. 5190919
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266	5	3.7	23	4	US-09-082-279B-1290	Sequence 1290, Ap	339	5	3.7	37	4	US-09-082-279B-1117	Sequence 1117, Ap
267	5	3.7	23	4	US-09-082-279B-1291	Sequence 1291, Ap	340	5	3.7	39	4	US-09-082-279B-1116	Sequence 1116, Ap
268	5	3.7	23	4	US-09-082-279B-1293	Sequence 1293, Ap	341	5	3.7	39	4	US-09-082-279B-1130	Sequence 1130, Ap
269	5	3.7	23	4	US-09-082-279B-1294	Sequence 1294, Ap	342	5	3.7	39	4	US-09-082-279B-1131	Sequence 1131, Ap
270	5	3.7	23	4	US-09-082-279B-1324	Sequence 1324, Ap	343	5	3.7	39	4	US-09-082-279B-1134	Sequence 1134, Ap
271	5	3.7	23	4	US-09-082-279B-1325	Sequence 1325, Ap	344	5	3.7	39	4	US-09-082-279B-1149	Sequence 1149, Ap
272	5	3.7	23	4	US-09-082-279B-1326	Sequence 1326, Ap	345	5	3.7	39	4	US-09-082-279B-1150	Sequence 1150, Ap
273	5	3.7	23	4	US-09-082-279B-1328	Sequence 1328, Ap	346	5	3.7	40	4	US-09-082-279B-1133	Sequence 1133, Ap
274	5	3.7	23	4	US-09-082-279B-1329	Sequence 1329, Ap	347	5	3.7	40	5	PCT-US93-05640-12	Sequence 12, Appli
275	5	3.7	24	6	5190919-16	Patent No. 5190919	348	5	3.7	40	5	PCT-US93-05640-23	Sequence 23, Appli
276	5	3.7	26	1	US-07-807-529A-9	Sequence 9, Appli	349	5	3.7	41	4	US-09-082-279B-1135	Sequence 1135, Ap
277	5	3.7	26	1	US-07-942-245-231	Sequence 231, App	350	5	3.7	42	4	US-09-082-279B-1132	Sequence 1132, Ap
278	5	3.7	26	1	US-07-942-245-232	Sequence 232, App	351	5	3.7	43	1	US-08-178-477B-22	Sequence 22, Appli
279	5	3.7	26	1	US-07-942-245-233	Sequence 233, App	352	5	3.7	43	2	US-08-210-762E-6	Sequence 6, Appli
280	5	3.7	26	1	US-07-942-245-234	Sequence 234, App	353	5	3.7	43	2	US-08-210-762E-17	Sequence 17, Appli
281	5	3.7	26	1	US-07-942-245-235	Sequence 235, App	354	5	3.7	43	2	US-08-488-161-38	Sequence 38, Appli
282	5	3.7	26	1	US-07-942-245-237	Sequence 237, App	355	5	3.7	43	3	US-09-273-685-18	Sequence 38, Appli
283	5	3.7	26	1	US-07-942-245-238	Sequence 238, App	356	5	3.7	43	4	US-09-015-030-7	Sequence 7, Appli
284	5	3.7	26	1	US-07-942-245-239	Sequence 239, App	357	5	3.7	43	5	PCT-US95-11334-38	Sequence 38, Appli
285	5	3.7	26	1	US-07-942-245-240	Sequence 240, App	358	5	3.7	44	4	US-09-046-894-41	Sequence 41, Appli
286	5	3.7	26	1	US-07-942-245-241	Sequence 241, App	359	5	3.7	44	4	US-09-046-894-42	Sequence 42, Appli
287	5	3.7	26	1	US-07-942-245-244	Sequence 244, App	360	5	3.7	45	1	US-08-664-856A-2	Sequence 2, Appli
288	5	3.7	26	1	US-07-942-245-247	Sequence 247, App	361	5	3.7	45	1	US-08-801-765-2	Sequence 2, Appli
289	5	3.7	26	1	US-07-942-245-248	Sequence 248, App	362	5	3.7	45	2	US-08-931-877-2	Sequence 2, Appli
290	5	3.7	26	1	US-07-942-245-249	Sequence 249, App	363	5	3.7	45	2	US-08-664-857A-2	Sequence 2, Appli
291	5	3.7	26	1	US-07-942-245-250	Sequence 250, App	364	5	3.7	45	3	US-09-069-484-2	Sequence 2, Appli
292	5	3.7	26	1	US-07-942-245-252	Sequence 252, App	365	5	3.7	45	4	US-09-135-599-2	Sequence 2, Appli
293	5	3.7	26	1	US-07-942-245-253	Sequence 253, App	366	5	3.7	45	4	US-08-905-223-367	Sequence 367, App
294	5	3.7	26	1	US-07-942-245-254	Sequence 254, App	367	5	3.7	45	4	US-08-711-417C-179	Sequence 179, App
295	5	3.7	26	1	US-07-942-245-260	Sequence 260, App	368	5	3.7	45	4	US-08-711-417C-181	Sequence 181, App
296	5	3.7	26	1	US-07-942-245-261	Sequence 261, App	369	5	3.7	45	4	US-09-369-744-2	Sequence 2, Appli
297	5	3.7	26	1	US-07-942-245-269	Sequence 269, App	370	5	3.7	50	1	US-07-956-700B-55	Sequence 55, Appli
298	5	3.7	26	1	US-07-942-245-424	Sequence 424, App	371	5	3.7	50	1	US-08-476-537-55	Sequence 55, Appli
299	5	3.7	26	1	US-07-942-245-426	Sequence 426, App	372	5	3.7	50	1	US-08-485-607-55	Sequence 55, Appli
300	5	3.7	26	1	US-07-942-245-427	Sequence 427, App	373	5	3.7	50	2	US-08-475-879-55	Sequence 55, Appli
301	5	3.7	26	1	US-07-942-245-429	Sequence 429, App	374	5	3.7	54	1	US-08-165-038-1	Sequence 1, Appli
302	5	3.7	26	1	US-07-942-245-433	Sequence 433, App	375	5	3.7	54	1	US-08-621-081A-1	Sequence 1, Appli
303	5	3.7	26	1	US-07-942-245-434	Sequence 434, App	376	5	3.7	54	2	US-08-876-781-1	Sequence 1, Appli
304	5	3.7	26	1	US-07-942-245-437	Sequence 437, App	377	5	3.7	56	5	PCT-US92-08558-6	Sequence 6, Appli
305	5	3.7	26	1	US-07-942-245-445	Sequence 445, App	378	5	3.7	59	4	US-09-177-249-164	Sequence 164, App
306	5	3.7	26	1	US-07-942-245-446	Sequence 446, App	379	5	3.7	69	4	US-09-025-151-16	Sequence 16, App
307	5	3.7	26	1	US-07-942-245-447	Sequence 447, App	380	5	3.7	70	2	US-08-210-762E-16	Sequence 16, Appli
308	5	3.7	26	1	US-07-942-245-449	Sequence 449, App	381	5	3.7	72	4	US-08-836-500A-6	Sequence 6, Appli
309	5	3.7	26	1	US-07-942-245-451	Sequence 451, App	382	5	3.7	75	3	US-09-100-804-21	Sequence 21, Appli
310	5	3.7	26	3	US-08-300-928C-19	Sequence 19, Appli	383	5	3.7	78	2	US-08-469-412A-11	Sequence 11, Appli
311	5	3.7	26	3	US-08-430-944D-19	Sequence 19, Appli	384	5	3.7	78	4	US-09-021-715-11	Sequence 11, Appli
312	5	3.7	26	3	US-08-430-014-19	Sequence 19, Appli	385	5	3.7	79	2	US-08-469-412A-12	Sequence 12, Appli
313	5	3.7	26	3	US-08-431-184-19	Sequence 19, Appli	386	5	3.7	79	4	US-09-021-715-12	Sequence 12, Appli
314	5	3.7	26	5	PCT-US93-02462-9	Sequence 9, Appli	387	5	3.7	79	4	US-09-100-802-4	Sequence 4, Appli
315	5	3.7	28	4	US-09-248-588-41	Sequence 41, Appli	388	5	3.7	81	1	US-08-225-757B-8	Sequence 8, Appli
316	5	3.7	29	2	US-08-310-912A-17	Sequence 17, Appli	389	5	3.7	81	4	US-09-100-802-5	Sequence 5, Appli
317	5	3.7	29	3	US-08-841-089-17	Sequence 17, Appli	390	5	3.7	82	3	US-08-300-928C-16	Sequence 16, Appli
318	5	3.7	29	4	US-09-301-085-17	Sequence 17, Appli	391	5	3.7	82	3	US-08-430-944D-16	Sequence 16, Appli
319	5	3.7	29	5	PCT-US95-04570-17	Sequence 17, Appli	392	5	3.7	82	3	US-08-430-014-16	Sequence 16, Appli

393	5	3.7	82	3	US-08-431-184-16	Sequence 16, Appl	466	5	3.7	111	3	US-08-430-944D-6	Sequence 6, Appl
394	5	3.7	83	1	US-07-662-193-7	Sequence 7, Appl	467	5	3.7	111	3	US-08-430-014-6	Sequence 6, Appl
395	5	3.7	83	1	US-07-662-193-8	Sequence 8, Appl	468	5	3.7	111	3	US-08-881-037-20	Sequence 20, Appl
396	5	3.7	86	2	US-08-459-568-82	Sequence 82, Appl	469	5	3.7	111	3	US-08-431-184-6	Sequence 6, Appl
397	5	3.7	86	2	US-08-399-411-82	Sequence 82, Appl	470	5	3.7	111	3	US-08-637-647-15	Sequence 15, Appl
398	5	3.7	86	3	US-08-516-859A-82	Sequence 82, Appl	471	5	3.7	111	5	PCT-US95-17025-15	Sequence 15, Appl
399	5	3.7	87	3	US-08-554-840-17	Sequence 17, Appl	472	5	3.7	112	2	US-08-672-345C-107	Sequence 107, App
400	5	3.7	87	3	US-08-554-840-18	Sequence 18, Appl	473	5	3.7	113	4	US-09-214-095D-118	Sequence 118, App
401	5	3.7	87	3	US-08-554-840-20	Sequence 20, Appl	474	5	3.7	114	3	US-08-483-749A-10	Sequence 10, Appl
402	5	3.7	90	3	US-08-300-928C-14	Sequence 14, Appl	475	5	3.7	115	4	US-08-838-682-8	Sequence 8, Appl
403	5	3.7	90	3	US-08-430-944D-14	Sequence 14, Appl	476	5	3.7	115	4	US-08-895-914-8	Sequence 8, Appl
404	5	3.7	90	3	US-08-430-014-14	Sequence 14, Appl	477	5	3.7	115	4	US-09-357-710A-8	Sequence 8, Appl
405	5	3.7	90	3	US-08-431-184-14	Sequence 14, Appl	478	5	3.7	116	1	US-07-634-278-3	Sequence 3, Appl
406	5	3.7	90	4	US-09-334-601-23	Sequence 23, Appl	479	5	3.7	116	1	US-07-634-278-14	Sequence 14, Appl
407	5	3.7	90	4	US-09-334-601-24	Sequence 24, Appl	480	5	3.7	116	1	US-08-477-728-3	Sequence 3, Appl
408	5	3.7	91	4	US-09-334-601-25	Sequence 25, Appl	481	5	3.7	116	1	US-08-477-728-14	Sequence 14, Appl
409	5	3.7	91	4	US-09-234-553-1	Sequence 1, Appl	482	5	3.7	116	1	US-08-474-040-3	Sequence 3, Appl
410	5	3.7	92	1	US-08-307-499-31	Sequence 31, Appl	483	5	3.7	116	1	US-08-474-040-14	Sequence 14, Appl
411	5	3.7	92	1	US-08-290-448A-68	Sequence 68, Appl	484	5	3.7	116	1	US-08-487-200-3	Sequence 3, Appl
412	5	3.7	92	1	US-08-290-448A-68	Sequence 68, Appl	485	5	3.7	116	1	US-08-487-200-14	Sequence 14, Appl
413	5	3.7	92	1	US-08-175-069A-68	Sequence 68, Appl	486	5	3.7	116	1	US-08-488-113B-167	Sequence 167, App
414	5	3.7	92	2	US-08-721-488-6	Sequence 6, Appl	487	5	3.7	116	1	US-08-488-113B-168	Sequence 168, App
415	5	3.7	92	3	US-08-300-928C-13	Sequence 13, Appl	488	5	3.7	116	1	US-08-477-484B-167	Sequence 167, App
416	5	3.7	92	3	US-08-430-944D-13	Sequence 13, Appl	489	5	3.7	116	1	US-08-477-484B-168	Sequence 168, App
417	5	3.7	92	3	US-08-430-014-13	Sequence 13, Appl	490	5	3.7	116	1	US-08-107-668D-53	Sequence 53, Appl
418	5	3.7	92	3	US-08-431-184-13	Sequence 13, Appl	491	5	3.7	116	1	US-08-107-668D-54	Sequence 54, Appl
419	5	3.7	92	4	US-09-299-268-31	Sequence 31, Appl	492	5	3.7	116	1	US-08-472-788A-54	Sequence 54, Appl
420	5	3.7	93	3	US-09-208-804-3	Sequence 3, Appl	493	5	3.7	116	1	US-08-472-788A-85	Sequence 85, Appl
421	5	3.7	93	3	US-08-801-743-3	Sequence 3, Appl	494	5	3.7	116	1	US-08-690-102A-4	Sequence 4, Appl
422	5	3.7	94	1	US-08-290-448A-69	Sequence 69, Appl	495	5	3.7	116	2	US-08-477-531B-53	Sequence 53, Appl
423	5	3.7	94	1	US-08-290-448A-69	Sequence 69, Appl	496	5	3.7	116	2	US-08-477-531B-54	Sequence 54, Appl
424	5	3.7	94	1	US-08-175-069A-69	Sequence 69, Appl	497	5	3.7	116	2	US-08-646-360-167	Sequence 167, App
425	5	3.7	96	1	US-07-807-529A-39	Sequence 39, Appl	498	5	3.7	116	2	US-08-646-360-168	Sequence 168, App
426	5	3.7	96	3	US-08-430-944D-103	Sequence 103, App	499	5	3.7	116	2	US-08-082-842A-85	Sequence 85, Appl
427	5	3.7	96	3	US-08-431-184-103	Sequence 103, App	500	5	3.7	116	2	US-08-082-842A-85	Sequence 85, Appl
428	5	3.7	97	3	US-08-300-928C-10	Sequence 10, Appl	501	5	3.7	116	2	US-08-672-345C-17	Sequence 17, App
429	5	3.7	97	3	US-08-430-944D-10	Sequence 10, Appl	502	5	3.7	116	4	US-08-839-765-167	Sequence 167, App
430	5	3.7	97	3	US-08-430-014-10	Sequence 10, Appl	503	5	3.7	116	4	US-08-839-765-168	Sequence 168, App
431	5	3.7	97	3	US-08-431-184-10	Sequence 10, Appl	504	5	3.7	116	4	US-09-136-389-167	Sequence 167, App
432	5	3.7	100	4	US-08-851-843A-10	Sequence 10, Appl	505	5	3.7	116	4	US-09-136-389-168	Sequence 168, App
433	5	3.7	100	4	US-08-974-549A-192	Sequence 192, App	506	5	3.7	116	4	US-08-484-537-3	Sequence 3, Appl
434	5	3.7	100	4	US-08-854-050-10	Sequence 10, Appl	507	5	3.7	116	4	US-08-484-537-14	Sequence 14, Appl
435	5	3.7	102	2	US-08-911-319A-4	Sequence 4, Appl	508	5	3.7	116	4	US-09-127-902-4	Sequence 4, Appl
436	5	3.7	102	3	US-09-352-619-4	Sequence 4, Appl	509	5	3.7	116	4	US-09-155-107-4	Sequence 4, Appl
437	5	3.7	102	3	US-08-654-482-6	Sequence 6, Appl	510	5	3.7	116	4	US-09-214-095D-17	Sequence 17, Appl
438	5	3.7	108	4	US-08-436-463-15	Sequence 15, Appl	511	5	3.7	116	5	PCT-US95-09641-4	Sequence 4, Appl
439	5	3.7	108	2	US-08-672-345C-103	Sequence 103, App	512	5	3.7	117	2	US-08-290-592E-17	Sequence 17, Appl
440	5	3.7	108	2	US-08-888-366-6	Sequence 6, Appl	513	5	3.7	117	2	US-08-290-592E-18	Sequence 18, Appl
441	5	3.7	108	4	US-09-214-095D-110	Sequence 110, App	514	5	3.7	117	2	US-08-672-345C-13	Sequence 13, Appl
442	5	3.7	109	1	US-07-841-646-21	Sequence 21, Appl	515	5	3.7	117	2	US-08-814-806-4	Sequence 4, Appl
443	5	3.7	109	1	US-07-662-193-5	Sequence 5, Appl	516	5	3.7	117	4	US-09-214-095D-13	Sequence 13, Appl
444	5	3.7	109	1	US-07-901-703-17	Sequence 17, Appl	517	5	3.7	117	5	PCT-US95-10053-14	Sequence 14, Appl
445	5	3.7	109	1	US-08-147-023-21	Sequence 21, Appl	518	5	3.7	117	5	PCT-US95-10053-15	Sequence 15, Appl
446	5	3.7	109	1	US-07-807-529A-6	Sequence 6, Appl	519	5	3.7	117	5	PCT-US96-09448-17	Sequence 17, Appl
447	5	3.7	109	1	US-08-447-570-21	Sequence 21, Appl	520	5	3.7	117	5	PCT-US96-09448-18	Sequence 18, Appl
448	5	3.7	109	2	US-08-210-762E-22	Sequence 22, Appl	521	5	3.7	117	6	5514582-7	Patent No. 5514582
449	5	3.7	109	2	US-08-449-700-21	Sequence 21, Appl	522	5	3.7	118	2	US-08-116-247-10	Sequence 10, Appl
450	5	3.7	109	2	US-08-449-699A-21	Sequence 21, Appl	523	5	3.7	119	1	US-08-192-102-5	Sequence 5, Appl
451	5	3.7	109	3	US-08-300-928C-8	Sequence 8, Appl	524	5	3.7	119	1	US-08-324-799-5	Sequence 5, Appl
452	5	3.7	109	3	US-09-053-197A-16	Sequence 16, Appl	525	5	3.7	119	1	US-08-497-312-20	Sequence 20, Appl
453	5	3.7	109	3	US-08-430-944D-8	Sequence 8, Appl	526	5	3.7	119	1	US-08-667-769A-15	Sequence 15, Appl
454	5	3.7	109	3	US-08-430-014-8	Sequence 8, Appl	527	5	3.7	119	1	US-08-340-536A-12	Sequence 12, Appl
455	5	3.7	109	3	US-08-431-184-8	Sequence 8, Appl	528	5	3.7	119	1	US-08-340-536A-13	Sequence 13, Appl
456	5	3.7	109	3	US-09-202-181-2	Sequence 2, Appl	529	5	3.7	119	2	US-08-303-569B-15	Sequence 15, Appl
457	5	3.7	109	4	PCT-US93-02462-6	Sequence 6, Appl	530	5	3.7	119	2	US-08-303-569B-16	Sequence 16, Appl
458	5	3.7	109	5	PCT-US93-05446-17	Sequence 17, Appl	531	5	3.7	119	2	US-08-303-569B-18	Sequence 18, Appl
459	5	3.7	111	1	US-07-662-193-4	Sequence 4, Appl	532	5	3.7	119	2	US-08-303-569B-15	Sequence 15, Appl
460	5	3.7	111	1	US-08-467-420A-15	Sequence 15, Appl	533	5	3.7	119	2	US-08-303-569B-16	Sequence 16, Appl
461	5	3.7	111	1	US-08-470-110A-15	Sequence 15, Appl	534	5	3.7	119	2	US-08-303-569B-17	Sequence 17, Appl
462	5	3.7	111	1	US-08-369-796-15	Sequence 15, Appl	535	5	3.7	119	2	US-08-303-569B-18	Sequence 18, Appl
463	5	3.7	111	2	US-08-940-371-15	Sequence 15, Appl	536	5	3.7	119	2	US-08-303-569B-19	Sequence 19, Appl
464	5	3.7	111	2	US-08-852-091-15	Sequence 15, Appl	537	5	3.7	119	2	US-08-303-569B-20	Sequence 20, Appl
465	5	3.7	111	3	US-08-300-928C-6	Sequence 6, Appl	538	5	3.7	119	2	US-08-303-569B-20	Sequence 20, Appl

539	5	3.7	119	2	US-08-303-569B-21	Sequence 21, Appl	612	5	3.7	134	2	US-08-436-717-39	Sequence 39, Appl
540	5	3.7	119	2	US-08-303-569B-22	Sequence 22, Appl	613	5	3.7	134	2	US-08-822-028-10	Sequence 10, Appl
541	5	3.7	119	2	US-08-303-569B-23	Sequence 23, Appl	614	5	3.7	134	4	US-08-479-285-10	Sequence 10, Appl
542	5	3.7	119	2	US-08-303-569B-24	Sequence 24, Appl	615	5	3.7	135	1	US-08-446-600A-4	Sequence 4, Appl
543	5	3.7	119	2	US-08-303-569B-30	Sequence 30, Appl	616	5	3.7	135	4	US-08-579-378A-16	Sequence 16, Appl
544	5	3.7	119	2	US-08-070-116A-10	Sequence 10, Appl	617	5	3.7	136	3	US-09-184-658-32	Sequence 32, Appl
545	5	3.7	119	2	US-08-192-861A-5	Sequence 5, Appl	618	5	3.7	136	3	US-08-649-100-25	Sequence 25, Appl
546	5	3.7	119	2	US-08-116-247-12	Sequence 12, Appl	619	5	3.7	137	2	US-08-379-057-18	Sequence 18, Appl
547	5	3.7	119	2	US-08-116-247-13	Sequence 13, Appl	620	5	3.7	137	2	US-08-621-751A-4	Sequence 1, Appl
548	5	3.7	119	2	US-08-116-247-14	Sequence 14, Appl	621	5	3.7	137	2	US-08-640-978C-1	Sequence 1, Appl
549	5	3.7	119	2	US-08-116-247-15	Sequence 15, Appl	622	5	3.7	137	2	US-08-640-978C-5	Sequence 5, Appl
550	5	3.7	119	2	US-08-116-247-16	Sequence 16, Appl	623	5	3.7	137	2	US-08-836-561-31	Sequence 31, Appl
551	5	3.7	119	2	US-08-116-247-17	Sequence 17, Appl	624	5	3.7	137	4	US-09-091-117-4	Sequence 4, Appl
552	5	3.7	119	2	US-08-116-247-18	Sequence 18, Appl	625	5	3.7	139	1	US-08-330-978-2	Sequence 2, Appl
553	5	3.7	119	2	US-08-116-247-19	Sequence 19, Appl	626	5	3.7	139	1	US-08-474-042-2	Sequence 2, Appl
554	5	3.7	119	2	US-08-116-247-20	Sequence 20, Appl	627	5	3.7	139	1	US-08-484-558-2	Sequence 2, Appl
555	5	3.7	119	2	US-08-116-247-21	Sequence 21, Appl	628	5	3.7	139	1	US-08-774-592-2	Sequence 2, Appl
556	5	3.7	119	2	US-08-116-247-22	Sequence 22, Appl	629	5	3.7	140	1	US-07-946-421-24	Sequence 24, Appl
557	5	3.7	119	2	US-08-116-247-23	Sequence 23, Appl	630	5	3.7	140	2	US-08-448-287-4	Sequence 2, Appl
558	5	3.7	119	2	US-08-116-247-24	Sequence 24, Appl	631	5	3.7	140	3	US-08-836-561-27	Sequence 27, Appl
559	5	3.7	119	2	US-08-116-247-25	Sequence 25, Appl	632	5	3.7	140	4	US-08-569-147-76	Sequence 76, Appl
560	5	3.7	119	2	US-08-767-128-18	Sequence 18, Appl	633	5	3.7	141	4	US-09-286-529-22	Sequence 22, Appl
561	5	3.7	119	4	US-09-133-119-5	Sequence 5, Appl	634	5	3.7	142	4	US-08-975-080-34	Sequence 34, Appl
562	5	3.7	119	4	US-08-192-093A-5	Sequence 5, Appl	635	5	3.7	143	1	US-08-236-520-7	Sequence 7, Appl
563	5	3.7	119	5	PCT-US95-17082A-15	Sequence 15, Appl	636	5	3.7	143	5	PCT-US95-05262-7	Sequence 7, Appl
564	5	3.7	120	1	US-08-111-080-25	Sequence 25, Appl	637	5	3.7	145	3	US-08-630-112-5	Sequence 5, Appl
565	5	3.7	120	1	US-08-211-980-25	Sequence 25, Appl	638	5	3.7	145	4	US-09-375-419-5	Sequence 5, Appl
566	5	3.7	120	1	US-08-497-312-26	Sequence 26, Appl	639	5	3.7	147	1	US-08-259-372A-8	Sequence 8, Appl
567	5	3.7	120	2	US-08-002-324-2	Sequence 2, Appl	640	5	3.7	147	1	US-08-468-671-8	Sequence 8, Appl
568	5	3.7	120	3	US-08-554-840-5	Sequence 5, Appl	641	5	3.7	149	3	US-08-584-031-17	Sequence 17, Appl
569	5	3.7	120	3	US-08-554-840-6	Sequence 6, Appl	642	5	3.7	150	2	US-08-400-115-2	Sequence 2, Appl
570	5	3.7	120	3	US-08-554-840-7	Sequence 7, Appl	643	5	3.7	158	1	US-08-403-866-8	Sequence 8, Appl
571	5	3.7	120	3	US-08-554-840-8	Sequence 8, Appl	644	5	3.7	158	4	US-08-836-075A-66	Sequence 66, Appl
572	5	3.7	120	4	US-09-188-930-180	Sequence 180, Appl	645	5	3.7	158	4	US-09-267-177-10	Sequence 10, Appl
573	5	3.7	120	5	PCT-US93-07967-25	Sequence 25, Appl	646	5	3.7	161	3	US-08-493-071-17	Sequence 17, Appl
574	5	3.7	120	5	PCT-US94-00261-2	Sequence 2, Appl	647	5	3.7	161	3	US-08-493-071-20	Sequence 20, Appl
575	5	3.7	121	1	US-08-339-582-2	Sequence 2, Appl	648	5	3.7	163	5	PCT-US91-02942-5	Sequence 5, Appl
576	5	3.7	121	1	US-08-974-889-4	Sequence 4, Appl	649	5	3.7	164	2	US-08-911-319A-1	Sequence 1, Appl
577	5	3.7	122	1	US-08-236-520-9	Sequence 9, Appl	650	5	3.7	164	3	US-09-352-619-1	Sequence 1, Appl
578	5	3.7	122	1	US-08-335-573-7	Sequence 7, Appl	651	5	3.7	168	1	US-08-460-739-5	Sequence 5, Appl
579	5	3.7	122	5	PCT-US95-05262-9	Sequence 9, Appl	652	5	3.7	171	2	US-08-417-495-24	Sequence 24, Appl
580	5	3.7	123	1	US-08-131-625B-17	Sequence 17, Appl	653	5	3.7	171	2	US-08-284-391B-24	Sequence 24, Appl
581	5	3.7	123	1	US-08-497-312-15	Sequence 15, Appl	654	5	3.7	171	3	US-08-463-903-20	Sequence 20, Appl
582	5	3.7	123	1	US-08-497-312-17	Sequence 17, Appl	655	5	3.7	171	4	US-09-218-950-24	Sequence 24, Appl
583	5	3.7	123	2	US-08-560-358E-28	Sequence 28, Appl	656	5	3.7	171	5	PCT-US92-01185-24	Sequence 24, Appl
584	5	3.7	123	2	US-08-799-464A-53	Sequence 13, Appl	657	5	3.7	171	5	PCT-US95-00454-24	Sequence 24, Appl
585	5	3.7	123	4	US-08-686-968C-11	Sequence 11, Appl	658	5	3.7	173	3	US-08-669-408B-8	Sequence 8, Appl
586	5	3.7	123	4	US-09-113-750A-42	Sequence 42, Appl	659	5	3.7	177	2	US-08-465-794-17	Sequence 17, Appl
587	5	3.7	123	5	PCT-US95-09927-13	Sequence 13, Appl	660	5	3.7	177	3	US-09-048-813-17	Sequence 17, Appl
588	5	3.7	123	5	PCT-US95-10904-19	Sequence 19, Appl	661	5	3.7	178	2	US-08-465-794-18	Sequence 18, Appl
589	5	3.7	123	5	PCT-US95-10904-53	Sequence 53, Appl	662	5	3.7	178	3	US-09-049-813-18	Sequence 18, Appl
590	5	3.7	123	5	PCT-US95-10904-55	Sequence 55, Appl	663	5	3.7	178	4	US-08-663-191A-4	Sequence 4, Appl
591	5	3.7	123	5	PCT-US95-10904-57	Sequence 57, Appl	664	5	3.7	179	3	US-08-649-100-9	Sequence 9, Appl
592	5	3.7	123	5	PCT-US95-10904-59	Sequence 59, Appl	665	5	3.7	179	4	US-08-836-500A-4	Sequence 4, Appl
593	5	3.7	123	5	PCT-US95-10904-61	Sequence 61, Appl	666	5	3.7	183	1	US-08-447-010-3	Sequence 3, Appl
594	5	3.7	124	4	US-08-751-359-14	Sequence 14, Appl	667	5	3.7	185	1	US-08-044-621D-36	Sequence 36, Appl
595	5	3.7	125	4	US-08-751-359-13	Sequence 13, Appl	668	5	3.7	185	1	US-08-044-621D-37	Sequence 37, Appl
596	5	3.7	126	2	US-08-244-205-15	Sequence 15, Appl	669	5	3.7	185	1	US-08-709-912-3	Sequence 3, Appl
597	5	3.7	126	4	US-08-751-359-11	Sequence 11, Appl	670	5	3.7	185	1	US-08-709-912-5	Sequence 5, Appl
598	5	3.7	126	4	US-08-751-359-12	Sequence 12, Appl	671	5	3.7	185	2	US-09-047-370-3	Sequence 3, Appl
599	5	3.7	126	5	PCT-US92-10284-15	Sequence 15, Appl	672	5	3.7	185	2	US-09-047-370-5	Sequence 5, Appl
600	5	3.7	130	3	US-08-838-682-4	Sequence 4, Appl	673	5	3.7	187	2	US-08-530-369B-19	Sequence 19, Appl
601	5	3.7	130	3	US-08-895-914-4	Sequence 4, Appl	674	5	3.7	187	3	US-08-493-071-16	Sequence 16, Appl
602	5	3.7	130	4	US-09-357-710A-4	Sequence 4, Appl	675	5	3.7	187	3	US-08-493-071-19	Sequence 19, Appl
603	5	3.7	132	4	US-08-434-000A-14	Sequence 14, Appl	676	5	3.7	188	2	US-08-484-993B-20	Sequence 20, Appl
604	5	3.7	132	4	US-09-312-157-14	Sequence 14, Appl	677	5	3.7	188	2	US-08-484-158B-20	Sequence 20, Appl
605	5	3.7	133	2	US-08-822-028-6	Sequence 6, Appl	678	5	3.7	188	2	US-08-484-596A-20	Sequence 20, Appl
606	5	3.7	133	2	US-08-822-028-30	Sequence 30, Appl	679	5	3.7	188	2	US-08-480-150A-20	Sequence 20, Appl
607	5	3.7	133	3	US-08-463-903-4	Sequence 4, Appl	680	5	3.7	188	3	US-08-458-731-20	Sequence 20, Appl
608	5	3.7	133	3	US-08-479-285-6	Sequence 6, Appl	681	5	3.7	188	3	US-08-149-223A-20	Sequence 20, Appl
609	5	3.7	133	4	US-08-479-285-30	Sequence 30, Appl	682	5	3.7	190	3	US-08-881-094-20	Sequence 20, Appl
610	5	3.7	133	6	5219996-17	Patent No. 5219996	683	5	3.7	191	2	US-08-290-665A-173	Sequence 173, App
611	5	3.7	134	1	US-08-137-117D-39	Sequence 39, Appl	684	5	3.7	191	5	PCT-US95-10398-173	Sequence 173, App

685	5	3.7	192	3	US-09-103-359-2	Sequence 2, Appl1	758	5	3.7	232	3	US-09-106-468-8	Sequence 8, Appl1
686	5	3.7	194	3	US-08-881-094-17	Sequence 17, Appl1	759	5	3.7	232	4	US-09-106-466A-8	Sequence 8, Appl1
687	5	3.7	196	4	US-09-383-586-11	Sequence 11, Appl1	760	5	3.7	232	4	US-09-106-467-8	Sequence 8, Appl1
688	5	3.7	200	1	US-07-855-412B-1	Sequence 1, Appl1	761	5	3.7	233	2	US-09-151-611-1	Sequence 1, Appl1
689	5	3.7	200	2	US-08-308-887A-1	Sequence 1, Appl1	762	5	3.7	233	4	US-09-370-102-1	Sequence 1, Appl1
690	5	3.7	200	3	US-08-881-094-1	Sequence 1, Appl1	763	5	3.7	234	4	US-08-944-483-46	Sequence 1, Appl1
691	5	3.7	200	3	US-08-881-094-19	Sequence 18, Appl1	764	5	3.7	235	2	US-08-716-301-10	Sequence 10, Appl1
692	5	3.7	202	3	US-08-881-094-19	Sequence 18, Appl1	765	5	3.7	236	3	US-08-493-071-15	Sequence 15, Appl1
693	5	3.7	208	1	US-08-315-695-21	Sequence 21, Appl1	766	5	3.7	236	3	US-08-493-071-15	Sequence 15, Appl1
694	5	3.7	210	4	US-08-961-083-36	Sequence 36, Appl1	767	5	3.7	237	2	US-08-469-537A-85	Sequence 85, Appl1
695	5	3.7	211	2	US-08-575-964-1	Sequence 1, Appl1	768	5	3.7	238	3	US-09-286-690-7	Sequence 7, Appl1
696	5	3.7	211	2	US-08-963-500-1	Sequence 1, Appl1	769	5	3.7	239	4	US-08-279-772A-8	Sequence 8, Appl1
697	5	3.7	212	1	US-08-158-353-2	Sequence 2, Appl1	770	5	3.7	239	4	US-08-902-486-11	Sequence 11, Appl1
698	5	3.7	212	2	US-08-924-759-14	Sequence 14, Appl1	771	5	3.7	242	2	US-08-663-310-9	Sequence 9, Appl1
699	5	3.7	212	3	US-09-248-335-14	Sequence 14, Appl1	772	5	3.7	242	2	US-09-006-491-9	Sequence 9, Appl1
700	5	3.7	213	3	US-08-104-445-3	Sequence 3, Appl1	773	5	3.7	242	4	US-09-335-919-9	Sequence 9, Appl1
701	5	3.7	213	1	US-08-319-621A-12	Sequence 12, Appl1	774	5	3.7	244	4	US-08-980-832-29	Sequence 29, Appl1
702	5	3.7	213	1	US-08-165-038-4	Sequence 4, Appl1	775	5	3.7	245	3	US-08-415-788-33	Sequence 33, Appl1
703	5	3.7	213	1	US-08-621-081A-4	Sequence 11, Appl1	776	5	3.7	245	3	US-09-286-690-2	Sequence 2, Appl1
704	5	3.7	213	2	US-08-311-525-11	Sequence 11, Appl1	777	5	3.7	246	4	US-09-216-295-20	Sequence 20, Appl1
705	5	3.7	213	2	US-08-876-781-4	Sequence 4, Appl1	778	5	3.7	248	2	US-08-755-559-1	Sequence 1, Appl1
706	5	3.7	213	2	US-08-718-270A-11	Sequence 11, Appl1	779	5	3.7	248	3	US-08-750-145A-18	Sequence 18, Appl1
707	5	3.7	217	1	US-08-621-081A-13	Sequence 13, Appl1	780	5	3.7	248	3	US-08-750-145A-20	Sequence 20, Appl1
708	5	3.7	217	1	US-08-621-081A-21	Sequence 21, Appl1	781	5	3.7	248	3	US-08-975-698A-22	Sequence 22, Appl1
709	5	3.7	217	1	US-08-621-081A-22	Sequence 22, Appl1	782	5	3.7	248	3	US-08-975-698A-24	Sequence 24, Appl1
710	5	3.7	217	1	US-08-621-081A-23	Sequence 23, Appl1	783	5	3.7	248	4	US-09-210-474-1	Sequence 1, Appl1
711	5	3.7	217	1	US-08-621-081A-24	Sequence 24, Appl1	784	5	3.7	248	4	US-09-417-090-22	Sequence 22, Appl1
712	5	3.7	217	1	US-08-621-081A-25	Sequence 25, Appl1	785	5	3.7	248	4	US-08-155-111B-32	Sequence 32, Appl1
713	5	3.7	217	1	US-08-621-081A-26	Sequence 26, Appl1	786	5	3.7	249	2	US-08-435-998-32	Sequence 32, Appl1
714	5	3.7	217	1	US-08-621-081A-27	Sequence 27, Appl1	787	5	3.7	249	2	US-08-750-145A-3	Sequence 3, Appl1
715	5	3.7	217	1	US-08-621-081A-28	Sequence 28, Appl1	788	5	3.7	249	3	US-08-750-145A-10	Sequence 10, Appl1
716	5	3.7	217	1	US-08-621-081A-29	Sequence 29, Appl1	789	5	3.7	249	3	US-08-975-698A-7	Sequence 7, Appl1
717	5	3.7	217	1	US-08-621-081A-29	Sequence 29, Appl1	790	5	3.7	249	3	US-08-975-698A-7	Sequence 7, Appl1
718	5	3.7	219	1	PCT-US94-14106-59	Sequence 59, Appl1	791	5	3.7	249	4	US-08-591-468-2	Sequence 2, Appl1
719	5	3.7	219	4	US-09-247-373B-52	Sequence 52, Appl1	792	5	3.7	249	4	US-09-417-090-7	Sequence 7, Appl1
720	5	3.7	221	4	US-08-621-081A-19	Sequence 19, Appl1	793	5	3.7	249	4	US-09-417-090-7	Sequence 7, Appl1
721	5	3.7	222	1	US-07-688-352C-46	Sequence 46, Appl1	794	5	3.7	249	4	US-09-446-504-1	Sequence 1, Appl1
722	5	3.7	222	1	US-09-248-335-66	Sequence 66, Appl1	795	5	3.7	249	4	PCT-US94-06430-2	Sequence 2, Appl1
723	5	3.7	222	5	PCT-US81-02714-43	Sequence 43, Appl1	796	5	3.7	252	3	US-08-279-772A-6	Sequence 6, Appl1
724	5	3.7	222	5	PCT-US91-02714-54	Sequence 54, Appl1	797	5	3.7	252	4	US-08-902-486-9	Sequence 9, Appl1
725	5	3.7	223	4	US-09-120-426-4	Sequence 4, Appl1	798	5	3.7	252	4	US-08-474-316-16	Sequence 16, Appl1
726	5	3.7	223	5	PCT-US94-14106-51	Sequence 51, Appl1	799	5	3.7	253	2	US-08-474-316-16	Sequence 16, Appl1
727	5	3.7	224	4	US-09-115-488-4	Sequence 4, Appl1	800	5	3.7	253	3	US-09-146-249A-46	Sequence 46, Appl1
728	5	3.7	224	4	US-08-448-398-1	Sequence 1, Appl1	801	5	3.7	253	3	US-08-206-188B-46	Sequence 46, Appl1
729	5	3.7	224	4	US-08-448-398-17	Sequence 17, Appl1	802	5	3.7	253	4	US-09-042-785A-4	Sequence 4, Appl1
730	5	3.7	224	4	US-08-447-703B-7	Sequence 7, Appl1	803	5	3.7	254	4	US-09-247-373B-38	Sequence 38, Appl1
731	5	3.7	225	4	US-09-247-373B-36	Sequence 36, Appl1	804	5	3.7	254	4	US-08-944-483-30	Sequence 30, Appl1
732	5	3.7	227	4	US-07-869-933-14	Sequence 14, Appl1	805	5	3.7	254	4	US-08-478-316-16	Sequence 16, Appl1
733	5	3.7	227	4	US-09-103-663-14	Sequence 14, Appl1	806	5	3.7	254	4	US-08-478-316-16	Sequence 16, Appl1
734	5	3.7	227	4	US-09-230-196-21	Sequence 21, Appl1	807	5	3.7	254	4	US-08-478-316-16	Sequence 16, Appl1
735	5	3.7	229	3	US-08-750-145A-4	Sequence 4, Appl1	808	5	3.7	255	5	PCT-US95-10904-69	Sequence 69, Appl1
736	5	3.7	229	3	US-08-975-698A-4	Sequence 4, Appl1	809	5	3.7	255	2	US-09-027-337-7	Sequence 7, Appl1
737	5	3.7	229	4	US-08-751-359-22	Sequence 22, Appl1	810	5	3.7	256	2	US-08-719-758-2	Sequence 2, Appl1
738	5	3.7	229	4	US-09-247-373B-48	Sequence 48, Appl1	811	5	3.7	256	4	US-09-119-827-2	Sequence 2, Appl1
739	5	3.7	229	4	US-09-417-090-4	Sequence 4, Appl1	812	5	3.7	261	1	US-07-940-605A-2	Sequence 2, Appl1
740	5	3.7	230	1	US-08-118-469A-3	Sequence 3, Appl1	813	5	3.7	261	1	US-08-184-422-8	Sequence 8, Appl1
741	5	3.7	230	1	US-08-909-119-3	Sequence 3, Appl1	814	5	3.7	261	1	US-08-360-923A-2	Sequence 2, Appl1
742	5	3.7	231	1	US-08-681-432-1	Sequence 11, Appl1	815	5	3.7	261	2	US-08-431-055-4	Sequence 4, Appl1
743	5	3.7	231	3	US-08-750-145A-11	Sequence 11, Appl1	816	5	3.7	261	2	US-08-690-99-12	Sequence 2, Appl1
744	5	3.7	231	3	US-08-975-698A-8	Sequence 8, Appl1	817	5	3.7	261	2	US-08-484-624A-12	Sequence 12, Appl1
745	5	3.7	231	3	US-09-417-090-8	Sequence 8, Appl1	818	5	3.7	261	2	US-08-477-733B-12	Sequence 12, Appl1
746	5	3.7	232	1	US-08-278-091-8	Sequence 8, Appl1	819	5	3.7	261	2	US-08-989-478-16	Sequence 16, Appl1
747	5	3.7	232	1	US-08-483-858-8	Sequence 8, Appl1	820	5	3.7	261	2	US-08-989-478-16	Sequence 16, Appl1
748	5	3.7	232	1	US-08-472-173-8	Sequence 8, Appl1	821	5	3.7	261	3	US-08-763-895-2	Sequence 3, Appl1
749	5	3.7	232	1	US-08-631-607-5	Sequence 5, Appl1	822	5	3.7	261	3	US-08-996-685-16	Sequence 2, Appl1
750	5	3.7	232	2	US-08-487-167-8	Sequence 8, Appl1	823	5	3.7	261	3	US-09-088-913A-12	Sequence 12, Appl1
751	5	3.7	232	2	US-08-482-816-8	Sequence 8, Appl1	824	5	3.7	261	3	US-08-589-371B-8	Sequence 8, Appl1
752	5	3.7	232	2	US-08-296-149-8	Sequence 8, Appl1	825	5	3.7	261	4	US-08-768-373-2	Sequence 2, Appl1
753	5	3.7	232	2	US-08-801-499-8	Sequence 8, Appl1	826	5	3.7	261	4	US-08-769-819-12	Sequence 12, Appl1
754	5	3.7	232	2	US-08-978-404B-45	Sequence 45, Appl1	827	5	3.7	261	4	US-08-770-974-14	Sequence 14, Appl1
755	5	3.7	232	2	US-08-615-271-8	Sequence 8, Appl1	828	5	3.7	261	5	US-08-858-197-4	Sequence 4, Appl1
756	5	3.7	232	3	US-09-074-660-8	Sequence 8, Appl1	829	5	3.7	261	5	PCT-US93-10034-4	Sequence 4, Appl1
757	5	3.7	232	3	US-09-074-659-8	Sequence 8, Appl1	830	5	3.7	262	2	US-08-719-697-10	Sequence 10, Appl1

831	5	3.7	262	4	US-08-154-364-41	Sequence 41, Appl	904	5	3.7	296	1	US-08-428-937-2	Sequence 2, Appl
832	5	3.7	262	4	US-08-727-616A-10	Sequence 10, Appl	905	5	3.7	296	1	US-08-428-298-2	Sequence 2, Appl
833	5	3.7	263	4	US-08-776-059-43	Sequence 43, Appl	906	5	3.7	296	1	US-08-339-517-2	Sequence 2, Appl
834	5	3.7	264	1	US-08-107-042-2	Sequence 24, Appl	907	5	3.7	296	2	US-08-438-863-5	Sequence 5, Appl
835	5	3.7	264	2	US-07-857-224B-24	Sequence 24, Appl	908	5	3.7	296	3	US-08-438-862-5	Sequence 5, Appl
836	5	3.7	264	4	US-08-776-059-33	Sequence 33, Appl	909	5	3.7	297	2	US-08-504-459-12	Sequence 12, Appl
837	5	3.7	268	4	US-09-085-305-10	Sequence 10, Appl	910	5	3.7	301	4	US-08-656-906-25	Sequence 25, Appl
838	5	3.7	270	2	US-08-652-507-2	Sequence 2, Appl	911	5	3.7	301	4	US-09-217-847-25	Sequence 25, Appl
839	5	3.7	271	2	US-08-400-115-4	Sequence 4, Appl	912	5	3.7	306	1	US-08-424-662A-1	Sequence 1, Appl
840	5	3.7	271	4	US-08-957-351-26	Sequence 26, Appl	913	5	3.7	308	2	US-08-807-050-4	Sequence 4, Appl
841	5	3.7	273	1	US-08-446-922-11	Sequence 11, Appl	914	5	3.7	310	1	US-08-129-456A-37	Sequence 37, Appl
842	5	3.7	273	2	US-08-249-189-21	Sequence 21, Appl	915	5	3.7	311	1	US-07-701-935-26	Sequence 26, Appl
843	5	3.7	273	2	US-08-484-624A-21	Sequence 21, Appl	916	5	3.7	312	2	US-09-014-969-17	Sequence 17, Appl
844	5	3.7	273	3	US-08-477-733B-21	Sequence 21, Appl	917	5	3.7	312	4	US-08-360-821B-36	Sequence 36, Appl
845	5	3.7	273	3	US-09-088-913A-21	Sequence 21, Appl	918	5	3.7	315	2	US-08-910-927B-3	Sequence 3, Appl
846	5	3.7	273	4	US-08-769-819-21	Sequence 21, Appl	919	5	3.7	315	4	US-09-270-270-3	Sequence 3, Appl
847	5	3.7	273	4	US-08-770-974-21	Sequence 21, Appl	920	5	3.7	316	1	US-07-805-567-2	Sequence 2, Appl
848	5	3.7	275	3	US-08-463-903-6	Sequence 6, Appl	921	5	3.7	316	4	US-08-961-083-156	Sequence 156, App
849	5	3.7	277	1	US-08-690-457-5	Sequence 5, Appl	922	5	3.7	319	2	US-08-977-847-1	Sequence 1, Appl
850	5	3.7	277	2	US-08-628-187-5	Sequence 5, Appl	923	5	3.7	319	2	US-09-195-021-1	Sequence 1, Appl
851	5	3.7	277	3	US-08-493-071-3	Sequence 3, Appl	924	5	3.7	320	1	US-07-613-083B-1	Sequence 1, Appl
852	5	3.7	278	1	US-07-941-414-1	Sequence 1, Appl	925	5	3.7	320	2	US-08-933-750C-12	Sequence 12, Appl
853	5	3.7	278	1	US-08-249-377A-1	Sequence 1, Appl	926	5	3.7	320	4	US-09-234-613-12	Sequence 12, Appl
854	5	3.7	278	1	US-08-585-595-1	Sequence 1, Appl	927	5	3.7	323	4	US-09-237-543-6	Sequence 6, Appl
855	5	3.7	278	2	US-08-740-337-1	Sequence 1, Appl	928	5	3.7	323	6	5185254-4	Patent No. 5185254
856	5	3.7	278	3	US-09-184-658-47	Sequence 47, Appl	929	5	3.7	326	2	US-08-986-217-3	Sequence 3, Appl
857	5	3.7	278	3	US-09-260-283-2	Sequence 2, Appl	930	5	3.7	328	1	US-08-265-087-2	Sequence 2, Appl
858	5	3.7	279	1	US-08-690-457-11	Sequence 11, Appl	931	5	3.7	328	1	US-08-186-529-2	Sequence 2, Appl
859	5	3.7	279	2	US-08-628-187-11	Sequence 11, Appl	932	5	3.7	328	1	US-08-621-493-2	Sequence 2, Appl
860	5	3.7	279	3	US-08-493-071-6	Sequence 6, Appl	933	5	3.7	328	1	US-08-640-386A-2	Sequence 2, Appl
861	5	3.7	279	5	PCT-US95-00362-5	Sequence 5, Appl	934	5	3.7	328	2	US-08-965-688-2	Sequence 2, Appl
862	5	3.7	281	2	US-08-810-453-2	Sequence 2, Appl	935	5	3.7	328	2	US-08-751-767A-4	Sequence 4, Appl
863	5	3.7	281	4	US-08-815-190A-2	Sequence 2, Appl	936	5	3.7	328	4	US-09-260-173-2	Sequence 2, Appl
864	5	3.7	281	4	US-09-290-640-25	Sequence 25, Appl	937	5	3.7	331	1	US-08-364-081-3	Sequence 3, Appl
865	5	3.7	281	4	US-09-479-524-3	Sequence 3, Appl	938	5	3.7	331	1	US-08-630-552-3	Sequence 3, Appl
866	5	3.7	281	4	US-09-404-258-16	Sequence 16, Appl	939	5	3.7	331	5	PCT-US95-16558-3	Sequence 3, Appl
867	5	3.7	281	5	PCT-US95-00362-2	Sequence 2, Appl	940	5	3.7	334	1	US-08-287-442-9	Sequence 9, Appl
868	5	3.7	283	3	US-08-860-368B-21	Sequence 21, Appl	941	5	3.7	334	1	US-08-459-701-9	Sequence 9, Appl
869	5	3.7	283	4	US-08-961-083-124	Sequence 124, App	942	5	3.7	334	1	US-08-460-298-9	Sequence 9, Appl
870	5	3.7	284	3	US-09-053-197A-2	Sequence 2, Appl	943	5	3.7	334	1	US-08-459-174-9	Sequence 9, Appl
871	5	3.7	284	3	US-09-184-658-40	Sequence 40, Appl	944	5	3.7	334	4	US-08-711-417C-201	Sequence 201, App
872	5	3.7	284	4	US-08-793-701-39	Sequence 39, Appl	945	5	3.7	335	3	US-09-002-298-6	Sequence 6, Appl
873	5	3.7	284	4	US-08-793-701-41	Sequence 41, Appl	946	5	3.7	335	3	US-09-109-205-19	Sequence 19, Appl
874	5	3.7	284	4	US-08-793-701-57	Sequence 57, Appl	947	5	3.7	335	4	US-08-836-500A-2	Sequence 2, Appl
875	5	3.7	285	3	US-08-482-085B-20	Sequence 20, Appl	948	5	3.7	336	1	US-07-755-009-3	Sequence 3, Appl
876	5	3.7	285	3	US-08-463-903-22	Sequence 22, Appl	949	5	3.7	336	1	US-07-755-009-4	Sequence 4, Appl
877	5	3.7	285	4	US-09-095-855-197	Sequence 197, App	950	5	3.7	336	2	US-08-592-646A-1	Sequence 1, Appl
878	5	3.7	287	1	US-08-690-457-4	Sequence 4, Appl	951	5	3.7	336	2	US-08-474-379C-88	Sequence 88, Appl
879	5	3.7	287	2	US-08-628-187-4	Sequence 4, Appl	952	5	3.7	336	2	US-09-047-026A-2	Sequence 2, Appl
880	5	3.7	287	3	US-08-815-190A-16	Sequence 16, Appl	953	5	3.7	338	2	US-08-118-270-49	Sequence 49, Appl
881	5	3.7	287	3	US-08-493-071-2	Sequence 2, Appl	954	5	3.7	340	1	US-08-446-875-16	Sequence 16, Appl
882	5	3.7	287	4	US-09-097-767A-17	Sequence 17, Appl	955	5	3.7	340	2	US-08-446-875-2	Sequence 2, Appl
883	5	3.7	288	1	US-08-690-457-3	Sequence 3, Appl	956	5	3.7	340	4	US-09-360-779-2	Sequence 2, Appl
884	5	3.7	288	1	US-08-690-457-10	Sequence 10, Appl	957	5	3.7	343	3	PCT-US93-08528-49	Sequence 49, Appl
885	5	3.7	288	2	US-08-628-187-3	Sequence 3, Appl	958	5	3.7	343	2	US-08-446-875-2	Sequence 2, Appl
886	5	3.7	288	2	US-08-628-187-10	Sequence 10, Appl	959	5	3.7	343	2	US-09-123-851-1	Sequence 1, Appl
887	5	3.7	288	3	US-08-493-071-1	Sequence 1, Appl	960	5	3.7	343	2	US-08-102-385G-2	Sequence 2, Appl
888	5	3.7	288	3	US-08-493-071-5	Sequence 5, Appl	961	5	3.7	343	2	US-08-728-520-1	Sequence 1, Appl
889	5	3.7	289	1	US-08-690-457-9	Sequence 9, Appl	962	5	3.7	344	4	US-08-718-738-4	Sequence 4, Appl
890	5	3.7	289	2	US-08-628-187-9	Sequence 9, Appl	963	5	3.7	344	4	US-09-221-844-4	Sequence 4, Appl
891	5	3.7	289	3	US-08-493-071-4	Sequence 4, Appl	964	5	3.7	345	5	PCT-US95-03323A-4	Sequence 4, Appl
892	5	3.7	289	4	US-09-077-675A-10	Sequence 10, Appl	965	5	3.7	346	2	US-08-744-779A-2	Sequence 2, Appl
893	5	3.7	290	1	US-08-393-985-6	Sequence 6, Appl	966	5	3.7	346	2	US-08-862-531-2	Sequence 2, Appl
894	5	3.7	292	2	US-08-973-461A-4	Sequence 4, Appl	967	5	3.7	347	1	US-07-637-870-5	Sequence 5, Appl
895	5	3.7	292	3	US-08-648-010-4	Sequence 4, Appl	968	5	3.7	347	1	US-07-640-476-10	Sequence 10, Appl
896	5	3.7	293	2	US-08-489-141A-2	Sequence 2, Appl	969	5	3.7	348	1	US-09-094-557-3	Sequence 3, Appl
897	5	3.7	293	2	US-08-907-492A-4	Sequence 4, Appl	970	5	3.7	348	1	US-07-637-399-8	Sequence 8, Appl
898	5	3.7	293	2	US-08-576-626A-59	Sequence 59, Appl	971	5	3.7	348	2	US-08-112-703-8	Sequence 8, Appl
899	5	3.7	295	2	US-08-504-459-14	Sequence 14, Appl	972	5	3.7	348	3	US-08-974-546-1	Sequence 1, Appl
900	5	3.7	295	2	US-08-907-492A-2	Sequence 2, Appl	973	5	3.7	349	4	US-08-852-824-17	Sequence 17, Appl
901	5	3.7	296	1	US-08-428-926-2	Sequence 2, Appl	974	5	3.7	350	1	US-09-105-390-48	Sequence 48, Appl
902	5	3.7	296	1	US-08-435-434-5	Sequence 5, Appl	975	5	3.7	350	1	US-08-202-056-1	Sequence 1, Appl
903	5	3.7	296	1	US-08-435-436-5	Sequence 5, Appl	976	5	3.7	350	1	US-08-076-093A-2	Sequence 2, Appl
												US-08-450-393A-7	Sequence 7, Appl

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977 5 3.7 350 1 US-08-410-453A-1 Sequence 1, Appl1
978 5 3.7 350 1 US-08-701-265-2 Sequence 2, Appl1
979 5 3.7 350 1 US-08-410-454A-1 Sequence 1, Appl1
980 5 3.7 350 2 US-08-284-586-2 Sequence 2, Appl1
981 5 3.7 350 2 US-08-410-456A-1 Sequence 2, Appl1
982 5 3.7 350 2 US-08-805-478-2 Sequence 2, Appl1
983 5 3.7 350 2 US-08-802-627A-2 Sequence 2, Appl1
984 5 3.7 350 2 US-08-801-238-2 Sequence 2, Appl1
985 5 3.7 350 2 US-08-801-228-2 Sequence 2, Appl1
986 5 3.7 350 2 US-08-966-116-16 Sequence 16, Appl1
987 5 3.7 350 4 US-09-104-296-2 Sequence 2, Appl1
988 5 3.7 350 4 US-08-446-669-7 Sequence 2, Appl1
989 5 3.7 350 5 PCT-US95-00476-7 Sequence 7, Appl1
990 5 3.7 321 1 US-08-248-466B-12 Sequence 12, Appl1
991 5 3.7 332 2 US-08-967-272-2 Sequence 2, Appl1
992 5 3.7 333 2 US-08-865-203-4 Sequence 4, Appl1
993 5 3.7 333 2 US-07-849-420-4 Sequence 4, Appl1
994 5 3.7 333 4 US-09-253-854-4 Sequence 4, Appl1
995 5 3.7 353 4 US-08-855-424-4 Sequence 4, Appl1
996 5 3.7 354 1 US-07-759-568-2 Sequence 2, Appl1
997 5 3.7 354 3 US-08-969-644-10 Sequence 10, Appl1
998 5 3.7 354 3 US-08-444-189-10 Sequence 2, Appl1
999 5 3.7 354 4 US-09-068-569-2 Sequence 10, Appl1
1000 5 3.7 354 4 US-08-468-544-10 Sequence 10, Appl1
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ALIGNMENTS

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RESULT 1
US-08-371-505-2
; Sequence 2, Application US/08371505
; Patent No. 5695754
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; GENERAL INFORMATION:
; APPLICANT: COLLEN, DESIRE
; TITLE OF INVENTION: STAPHYLOKINASE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEBB ZIESENHEIM BRUENING LOGSDON ORKIN & HANSON, P.C.
; STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
; CITY: PITTSBURGH
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 15222-2363
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,505
; FILING DATE: 11 JAN 1995
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
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US-08-371-505-2
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Query Match 100.0%; Score 136; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.7e-133;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 SSSFDKGYKKGGDDASYEPTGPLYMNVNTGVDKGNELSPHYVEPIKPGTTLTKRKI 60
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DB 61 EYVEMALDATAVYKFRVVELDPSAKIEVYTYDKNKKKEETKSPITEKGFVVDLSSEHI 120
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OY 121 KNPGFNLTIVYIEKK 136
DB 121 KNPGFNLTIVYIEKK 136
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RESULT 2
US-08-784-971-5
; Sequence 5, Application US/087844971
; Patent No. 5951980
;
; GENERAL INFORMATION:
; APPLICANT: COLLEN, DESIRE
; TITLE OF INVENTION: NEW STAPHYLOKINASE DERIVATIVES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE WEBB LAW FIRM
; STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
; CITY: PITTSBURGH
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK
; COMPUTER: DIGITAL VENTURIS GL 6200
; OPERATING SYSTEM: DOS
; SOFTWARE: MICROSOFT WORD 2.0c
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,971
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/371,505
; FILING DATE: 11-JAN-1995
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
;
US-08-784-971-5
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Query Match 100.0%; Score 136; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.7e-133;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 SSSFDKGYKKGGDDASYEPTGPLYMNVNTGVDKGNELSPHYVEPIKPGTTLTKRKI 60
OY 61 EYVEMALDATAVYKFRVVELDPSAKIEVYTYDKNKKKEETKSPITEKGFVVDLSSEHI 120
DB 61 EYVEMALDATAVYKFRVVELDPSAKIEVYTYDKNKKKEETKSPITEKGFVVDLSSEHI 120
OY 121 KNPGFNLTIVYIEKK 136
DB 121 KNPGFNLTIVYIEKK 136
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RESULT 3
US-08-256-261-6
; Sequence 6, Application US/08256261
; Patent No. 5801037
;
; GENERAL INFORMATION:
; APPLICANT: Behnke, Detlef
; APPLICANT: Schlotz, Bernhard
; APPLICANT: Albrecht, Sybille
; APPLICANT: G hrs, Karl-Heinz
; APPLICANT: Hartmann, Manfred
; TITLE OF INVENTION: Expression of signal-peptide-free
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
```

```
;; ADDRESSEE: Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10020
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/256,261
;; FILING DATE:
;; CLASSIFICATION: 435
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 137 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-256-261-6
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Query Match          100.0%; Score 136; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.8e-133;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2 SSSFDKGGYKKGDASYPEPTGPIYLMVNVTVGDSKGNELLSPHYVEFPKPGTTLTKRKI 61
OY 61 EYVEMALDATAVKEFRVVELDPSAKIEVITYYDKNKKKEETKSPITEKGVPDLSSEHI 120
    |||||||
DB 62 EYVEMALDATAVKEFRVVELDPSAKIEVITYYDKNKKKEETKSPITEKGVPDLSSEHI 121
OY 121 KNPGFNLTIKVIEKK 136
    |||||||
DB 122 KNPGFNLTIKVIEKK 137
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```
RESULT 4
US-08-852-299-6
;; Sequence 6, Application US/08852299
;; Patent No. 6010897
;; GENERAL INFORMATION:
;; APPLICANT: Behnke, Detlef
;; APPLICANT: Schlott, Bernhard
;; APPLICANT: Albrecht, Sybille
;; APPLICANT: G hrs, Karl-Heinz
;; APPLICANT: Hartmann, Manfred
;; TITLE OF INVENTION: Expression of signal-peptide-free
;; TITLE OF INVENTION: staphylokinases
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10020
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/852,299
;; FILING DATE: 17-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/256,261
;; FILING DATE:
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;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 137 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-852-299-6
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Query Match          100.0%; Score 136; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.8e-133;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||||
DB 2 SSSFDKGGYKKGDASYPEPTGPIYLMVNVTVGDSKGNELLSPHYVEFPKPGTTLTKRKI 61
OY 61 EYVEMALDATAVKEFRVVELDPSAKIEVITYYDKNKKKEETKSPITEKGVPDLSSEHI 120
    |||||||
DB 62 EYVEMALDATAVKEFRVVELDPSAKIEVITYYDKNKKKEETKSPITEKGVPDLSSEHI 121
OY 121 KNPGFNLTIKVIEKK 136
    |||||||
DB 122 KNPGFNLTIKVIEKK 137
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RESULT 5
US-08-256-261-4
;; Sequence 4, Application US/08256261
;; Patent No. 5801037
;; GENERAL INFORMATION:
;; APPLICANT: Behnke, Detlef
;; APPLICANT: Schlott, Bernhard
;; APPLICANT: Albrecht, Sybille
;; APPLICANT: G hrs, Karl-Heinz
;; APPLICANT: Hartmann, Manfred
;; TITLE OF INVENTION: Expression of signal-peptide-free
;; TITLE OF INVENTION: staphylokinases
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10020
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/256,261
;; FILING DATE:
;; CLASSIFICATION: 435
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 137 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-256-261-4
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Query Match          75.0%; Score 102; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 6.1e-98;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 36 KGNELLSPHYVEFPKPGTTLTKRKIEYVEMALDATAVKEFRVVELDPSAKIEVITYYDK 95
OY 95 NKKKEETKSPITEKGVPDLSSEHIKNPGFNLTIKVIEKK 136
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Db 96 NKKKETKSPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 137

RESULT 6

US-08-852-299-4

Sequence 4, Application US/08852299

Patent No. 6010897

GENERAL INFORMATION:

APPLICANT: Behnke, Detlef

APPLICANT: Albrecht, Bernhard

APPLICANT: Albrecht, Sybille

APPLICANT: G hrs, Karl-Heinz

APPLICANT: Hartmann, Manfred

TITLE OF INVENTION: Expression of signal-peptide-free

TITLE OF INVENTION: staphylokinases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,299

FILING DATE: 17-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,261

FILING DATE:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-852-299-4

Query Match 75.0%; Score 102; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 6.1e-98;

Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 36 KKNELISPHYVEPIKPGTTLTKETIEYVEMALDATTAKKFRVVELDPSAKIEVTYYDK 95

QY 95 NKKKETKSPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136

Db 96 NKKKETKSPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 137

RESULT 7

US-08-256-261-10

Sequence 10, Application US/08256261

Patent No. 5801037

GENERAL INFORMATION:

APPLICANT: Behnke, Detlef

APPLICANT: Schloft, Bernhard

APPLICANT: Albrecht, Sybille

APPLICANT: G hrs, Karl-Heinz

APPLICANT: Hartmann, Manfred

TITLE OF INVENTION: Expression of signal-peptide-free

TITLE OF INVENTION: staphylokinases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,261

FILING DATE:

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-256-261-10

Query Match 68.4%; Score 93; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEPIKPGTTLTKETIEYVEMALDATTAKKFRVVELDPSAKIEVTYYDKNKKKEETKS 103

Db 31 YVEPIKPGTTLTKETIEYVEMALDATTAKKFRVVELDPSAKIEVTYYDKNKKKEETKS 90

QY 104 FTTEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136

Db 91 FTTEKGFVVPDLSEHIKNPGFNLTIKVIEKK 123

RESULT 8

US-08-852-299-10

Sequence 10, Application US/08852299

Patent No. 6010897

GENERAL INFORMATION:

APPLICANT: Behnke, Detlef

APPLICANT: Albrecht, Bernhard

APPLICANT: Albrecht, Sybille

APPLICANT: G hrs, Karl-Heinz

APPLICANT: Hartmann, Manfred

TITLE OF INVENTION: Expression of signal-peptide-free

TITLE OF INVENTION: staphylokinases

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,299

FILING DATE: 17-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,261

FILING DATE:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-852-299-10

Query Match
Best Local Similarity 68.4%; Score 93; DB 3; Length 123;
Matches 93: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 103
DB 31 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 90

QY 104 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136
DB 91 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 123

RESULT 9
US-08-256-261-8
Sequence 8, Application US/08256261
Patent No. 5801037
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schlotz, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-8

Query Match
Best Local Similarity 68.4%; Score 93; DB 1; Length 127;
Matches 93: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 103
DB 35 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 94

QY 104 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136
DB 95 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 127

RESULT 10
US-08-852-299-8
Sequence 8, Application US/08852299
Patent No. 6010897
GENERAL INFORMATION:

APPLICANT: Behnke, Detlef
APPLICANT: Schlotz, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-08-852-299-8

Query Match
Best Local Similarity 68.4%; Score 93; DB 3; Length 127;
Matches 93: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 103
DB 35 YVEFPKPGTTLTKKEIEYVEMALDATAKKEFRVVELDPSAKIEVYTDKNNKKEETS 94

QY 104 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136
DB 95 FPITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 127

RESULT 11
US-08-256-261-2
Sequence 2, Application US/08256261
Patent No. 5801037
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schlotz, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-2

Query Match 68.4%; Score 93; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 103
DB 45 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 104
QY 104 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 136
DB 105 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 137

RESULT 12
US-08-256-261-12
Sequence 12, Application US/08256261
Patent No. 5801037
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schloft, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-12

Query Match 68.4%; Score 93; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 103
DB 45 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 104

QY 104 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 136
DB 105 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 137

RESULT 13
US-08-256-261-14
Sequence 14, Application US/08256261
Patent No. 5801037
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schloft, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,261
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-261-14

Query Match 68.4%; Score 93; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 103
DB 45 YVEFPKPGTTLTKKEIEYVEMALDATAVKEFRVVELDPSAKIEVYYDKNKKKEETKS 104
QY 104 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 136
DB 105 FPIITEKGFVVPDLSEHKNGFNLTITKVIEKK 137

RESULT 14
US-08-852-299-2
Sequence 2, Application US/08852299
Patent No. 6010897
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schloft, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,299
FILING DATE: 17-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,261
FILING DATE:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-299-2

Query Match 68.4%; Score 93; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAYKEFRVVELDPSAKIEVITYYDKNKKKEETKS 103
|||||
DB 45 YVEFPKPGTTLTKKEIEYVEMALDATAYKEFRVVELDPSAKIEVITYYDKNKKKEETKS 104

QY 104 FPITEKGFVVDLSEHIKNGFNLTITKVIEKK 136
|||||
DB 105 FPITEKGFVVDLSEHIKNGFNLTITKVIEKK 137

RESULT 15
US-08-852-299-12
Sequence 12, Application US/08852299
Patent No. 6010897
GENERAL INFORMATION:
APPLICANT: Behnke, Detlef
APPLICANT: Schlotz, Bernhard
APPLICANT: Albrecht, Sybille
APPLICANT: G hrs, Karl-Heinz
APPLICANT: Hartmann, Manfred
TITLE OF INVENTION: Expression of signal-peptide-free
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,299
FILING DATE: 17-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,261
FILING DATE:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-299-12

Query Match 68.4%; Score 93; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEFPKPGTTLTKKEIEYVEMALDATAYKEFRVVELDPSAKIEVITYYDKNKKKEETKS 103
|||||
DB 45 YVEFPKPGTTLTKKEIEYVEMALDATAYKEFRVVELDPSAKIEVITYYDKNKKKEETKS 104

QY 104 FPITEKGFVVDLSEHIKNGFNLTITKVIEKK 136
|||||
DB 105 FPITEKGFVVDLSEHIKNGFNLTITKVIEKK 137

Search completed: April 22, 2002, 10:45:41
Job time: 116 sec

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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:44:00 ; Search time 14.45 Seconds

(without alignments)
716.937 Million cell updates/sec

Title: US-09-601-490-1

Perfect score: 136
Sequence: 1 SSSFPDKGKYKKGGDASYEP.....SEHIKNPGENLTRKVIIEKK 136

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: PIR.68.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	75.0	163	1 PRSAK	staphylokinase - p
2	93	68.4	163	2 S02330	staphylokinase - p
3	8	5.9	245	3 A72218	gufl protein - The
4	7	5.1	56	2 G69044	hypothetical prote
5	7	5.1	90	2 I46953	CGMP-gated retinal
6	7	5.1	92	2 P00629	coat protein - tul
7	7	5.1	102	2 C84026	ribosomal protein
8	7	5.1	138	2 D83704	transposase (14) B
9	7	5.1	194	2 E71501	hypothetical prote
10	7	5.1	204	2 D84190	tryptophan synthas
11	7	5.1	219	2 T27336	hypothetical prote
12	7	5.1	277	2 A56044	tryptophan synthas
13	7	5.1	288	2 S21499	coat protein - tur
14	7	5.1	288	2 S51329	polypotein - tur
15	7	5.1	311	2 A83746	transposase (16) B
16	7	5.1	334	2 T47256	thioredoxin reduct
17	7	5.1	337	2 A48347	coat protein - tur
18	7	5.1	343	2 E72694	hypothetical prote
19	7	5.1	371	2 C83736	transposase (15) B
20	7	5.1	388	2 P00757	polypotein - tur
21	7	5.1	388	2 P00759	polypotein - tur
22	7	5.1	398	2 T72335	hypothetical prote
23	7	5.1	399	2 T32933	hypothetical prote
24	7	5.1	408	2 S11689	coat protein - tur
25	7	5.1	424	2 T29158	hypothetical prote
26	7	5.1	694	2 A75127	hypothetical prote
27	7	5.1	722	2 S64492	hypothetical prote
28	7	5.1	944	2 H64650	translation initia
29	7	5.1	1008	2 T18508	hypothetical prote

30	7	5.1	1032	2 S12153	pol polypotein -
31	7	5.1	1034	1 GNLJCA	pol polypotein -
32	7	5.1	1035	1 GNLJG6	pol polypotein -
33	7	5.1	1036	1 GNLJG2	pol polypotein -
34	7	5.1	1055	1 GNLJST	pol polypotein -
35	7	5.1	1055	2 S53092	pol polypotein -
36	7	5.1	3163	1 U01895	genome polypotein
37	6	4.4	63	2 G69941	hypothetical prote
38	6	4.4	70	2 A31940	microtubule-associ
39	6	4.4	77	2 H82017	pseudogene (151655
40	6	4.4	85	2 S44604	C02F5.2 protein -
41	6	4.4	89	2 T45510	probable transport
42	6	4.4	90	2 P00292	polypotein - glori
43	6	4.4	129	1 A56623	hypothetical prote
44	6	4.4	129	2 C85946	glycine cleavage s
45	6	4.4	138	1 RKKKSC	hypothetical prote
46	6	4.4	138	1 RKKKSC	ribulose-bisphosph
47	6	4.4	138	2 D72420	hypothetical prote
48	6	4.4	141	2 H86609	kinase [imported]
49	6	4.4	146	2 E83190	(38)-hydroxymyrist
50	6	4.4	146	2 T33016	hypothetical prote
51	6	4.4	153	1 S08619	formate hydrogely
52	6	4.4	153	2 F43868	hypothetical prote
53	6	4.4	153	2 D85921	hypothetical prote
54	6	4.4	158	2 S78249	ribosomal protein
55	6	4.4	158	2 F83861	hypothetical prote
56	6	4.4	160	2 D70364	ribosomal protein
57	6	4.4	160	2 G70457	ribosomal protein
58	6	4.4	162	2 S13195	ganglioside M2 act
59	6	4.4	162	2 F86690	hypothetical prote
60	6	4.4	165	2 T52114	probable transcrip
61	6	4.4	166	2 B70369	cytochrome c552 -
62	6	4.4	166	2 G85057	hypothetical prote
63	6	4.4	173	2 JC5610	toponin I - sea s
64	6	4.4	175	2 A46388	Her-1 protein - Ca
65	6	4.4	175	2 D83304	conserved hypotet
66	6	4.4	183	1 C69474	conserved hypotet
67	6	4.4	187	2 G70226	conserved hypotet
68	6	4.4	191	2 H84472	hypothetical prote
69	6	4.4	193	2 I54178	ganglioside M2 act
70	6	4.4	199	2 G81261	probable lipoprote
71	6	4.4	200	2 S22411	ganglioside M2 act
72	6	4.4	200	2 D86645	hypothetical prote
73	6	4.4	201	2 E84187	hypothetical prote
74	6	4.4	210	2 F70546	hypothetical prote
75	6	4.4	215	2 T23482	hypothetical prote
76	6	4.4	216	2 T29842	hypothetical prote
77	6	4.4	216	2 T34527	hypothetical prote
78	6	4.4	219	2 A35650	Sur protein - chic
79	6	4.4	221	1 A26753	glutathione trans
80	6	4.4	223	1 A41031	hypothetical prote
81	6	4.4	226	1 D83875	hypothetical prote
82	6	4.4	227	2 A71224	probable fibrillar
83	6	4.4	227	2 H75191	fibrillar-like p
84	6	4.4	227	2 T41133	hypothetical prote
85	6	4.4	230	2 A40085	ubiquitin thiolest
86	6	4.4	230	2 JC7117	ubiquitin carboxy-
87	6	4.4	230	2 T34854	hypothetical prote
88	6	4.4	231	2 F70219	thiol-disulfide in
89	6	4.4	231	2 E81215	hypothetical prote
90	6	4.4	232	2 T29841	hypothetical prote
91	6	4.4	234	1 A70549	probable methyltra
92	6	4.4	237	2 C84968	cell division inh
93	6	4.4	240	2 S36797	lectin BMA - Bowri
94	6	4.4	241	2 B69655	two-component resp
95	6	4.4	244	2 T48110	hypothetical prote
96	6	4.4	248	2 E64898	H repeat-associate
97	6	4.4	252	2 E75491	time protein - Del
98	6	4.4	254	2 D82124	vacu lipoprotein V
99	6	4.4	265	2 S60947	hypothetical prote
100	6	4.4	269	1 A27067	calretinin - chick
101	6	4.4	269	2 F85063	hypothetical prote
102	6	4.4	270	2 T06992	translation initia

103	6	4.4	270	2	T35365	hypothetical prote
104	6	4.4	271	1	JX0316	phosphatidylinosit
105	6	4.4	272	2	T19537	hypothetical prote
106	6	4.4	274	2	T05864	hypothetical prote
107	6	4.4	275	2	E83655	signal peptidase-1
108	6	4.4	275	2	D70737	hypothetical prote
109	6	4.4	275	2	G85536	SKM dependent meth
110	6	4.4	276	2	D72066	sam dependent meth
111	6	4.4	276	2	T46368	hypothetical prote
112	6	4.4	277	2	G71849	amino acid ABC tra
113	6	4.4	279	2	A82922	conserved hypotet
114	6	4.4	279	2	F70612	hypothetical prote
115	6	4.4	279	2	C70101	hypothetical prote
116	6	4.4	281	2	H64125	modb protein homol
117	6	4.4	282	2	T31941	hypothetical prote
118	6	4.4	283	2	S10773	2-hydroxymuconic s
119	6	4.4	285	2	C45691	main capsid protei
120	6	4.4	292	2	F71901	hypothetical prote
121	6	4.4	292	2	E64614	beta-alanine synth
122	6	4.4	295	2	T34774	hypothetical prote
123	6	4.4	297	2	E69152	formylmethanofuran
124	6	4.4	299	2	H71976	probable alpha(1,2
125	6	4.4	301	2	A83653	acetylcholinestera
126	6	4.4	301	2	S62087	hrpF protein - Pse
127	6	4.4	302	2	G84053	hybrid-endo-beta-1
128	6	4.4	303	2	A25095	nodulation protei
129	6	4.4	304	2	T23919	hypothetical prote
130	6	4.4	313	2	S26838	nodulation protei
131	6	4.4	316	2	E82266	trehalose operon r
132	6	4.4	320	1	A43824	periplasmic flagel
133	6	4.4	321	2	G86400	hypothetical prote
134	6	4.4	331	2	E83839	hypothetical prote
135	6	4.4	332	2	A83857	3-dehydroquinatase
136	6	4.4	332	2	A48997	tumor surface anti
137	6	4.4	324	2	T25521	hypothetical prote
138	6	4.4	327	1	S75716	myoglobin cofacto
139	6	4.4	330	1	S15303	probable CDP-6-deo
140	6	4.4	331	2	T22648	hypothetical prote
141	6	4.4	332	2	T32863	hypothetical prote
142	6	4.4	340	2	S69194	N4-(beta-N-acetylgl
143	6	4.4	343	2	A75456	conserved hypotet
144	6	4.4	344	2	PC4185	hemagglutinin 1 ch
145	6	4.4	345	2	T37576	probable mitochond
146	6	4.4	345	2	S36080	hemagglutinin 1 -
147	6	4.4	345	2	JQ1308	hemagglutinin 1 -
148	6	4.4	345	2	JQ1309	hemagglutinin 1 -
149	6	4.4	345	2	JQ1913	hemagglutinin 1 -
150	6	4.4	345	2	JQ1906	hemagglutinin 1 -
151	6	4.4	345	2	JQ1915	hemagglutinin 1 -
152	6	4.4	345	2	JQ1916	hemagglutinin 1 -
153	6	4.4	345	2	JQ1911	hemagglutinin 1 -
154	6	4.4	345	2	JQ1914	hemagglutinin 1 -
155	6	4.4	345	2	JQ1912	hemagglutinin 1 -
156	6	4.4	345	2	JQ1907	hemagglutinin 1 -
157	6	4.4	345	2	JQ1910	hemagglutinin 1 -
158	6	4.4	347	2	JQ1901	hemagglutinin 1 -
159	6	4.4	347	2	JQ1904	hemagglutinin 1 -
160	6	4.4	347	2	JQ1902	hemagglutinin 1 -
161	6	4.4	347	2	JQ1905	hemagglutinin 1 -
162	6	4.4	347	2	JQ1903	hemagglutinin 1 -
163	6	4.4	348	2	A83532	hypothetical prote
164	6	4.4	349	2	D70383	hydrogenase (EC 1.
165	6	4.4	350	2	A75600	conserved hypotet
166	6	4.4	353	1	HMI1VA	hemagglutinin prec
167	6	4.4	361	2	T12571	clinnamyl-alcohol d
168	6	4.4	361	2	H71202	hypothetical prote
169	6	4.4	365	2	T08577	hypothetical prote
170	6	4.4	367	2	C84236	hypothetical prote
171	6	4.4	368	2	C70786	probable ilvE prot
172	6	4.4	373	2	G64840	hypothetical prote
173	6	4.4	375	2	S42434	hypothetical prote
174	6	4.4	375	2	B40205	Na+/H+-exchanging
175	6	4.4	376	2	E84742	hypothetical prote
176	6	4.4	376	2	T17128	hypothetical prote
177	6	4.4	377	1	S01615	site-specific DNA-
178	6	4.4	377	2	T40024	probable cytochrom
179	6	4.4	377	2	T21751	hypothetical prote
180	6	4.4	378	2	S11738	hemagglutinin prec
181	6	4.4	378	2	T18486	hypothetical prote
182	6	4.4	383	2	D75288	carbohydrate kinas
183	6	4.4	390	2	C85510	hypothetical prote
184	6	4.4	392	2	S04718	DNA-directed RNA p
185	6	4.4	392	2	A44167	aminomethyltransfe
186	6	4.4	396	2	S31151	translation elonga
187	6	4.4	396	2	E84186	cell division prot
188	6	4.4	396	2	A57030	CSA protein - huma
189	6	4.4	397	2	JC5385	translation elonga
190	6	4.4	398	2	JC4254	ribosomal protein
191	6	4.4	398	2	T15846	interleukin-1 rece
192	6	4.4	407	2	S17428	hypothetical prote
193	6	4.4	407	2	G84783	probable pectinest
194	6	4.4	407	2	F70451	hypothetical prote
195	6	4.4	409	2	F72504	probable 26S prote
196	6	4.4	410	2	A44391	serum response ele
197	6	4.4	412	2	G64685	hypothetical prote
198	6	4.4	412	2	S48881	rRNA (guanosine-2'
199	6	4.4	413	2	A69205	sensory transducti
200	6	4.4	414	1	C70859	probable hexosyltr
201	6	4.4	418	2	E96687	hypothetical prote
202	6	4.4	421	2	H72452	probable proton/so
203	6	4.4	424	2	T08412	hypothetical prote
204	6	4.4	424	2	E83384	probable ring-hydr
205	6	4.4	424	2	T31978	hypothetical prote
206	6	4.4	425	2	D75130	amino acid transpo
207	6	4.4	425	2	F71075	probable protein k
208	6	4.4	426	2	H84349	peroxidase / catal
209	6	4.4	426	2	S61186	glutamate 5-kinase
210	6	4.4	429	2	T32832	hypothetical prote
211	6	4.4	429	2	G82430	conserved hypotet
212	6	4.4	431	2	F69458	coenzyme F390 synt
213	6	4.4	433	2	D71309	47K integral membr
214	6	4.4	434	2	G84046	hypothetical prote
215	6	4.4	435	2	T27039	hypothetical prote
216	6	4.4	436	2	B70157	hypothetical prote
217	6	4.4	436	2	A64891	coenzyme F390 synt
218	6	4.4	437	2	T22060	hypothetical prote
219	6	4.4	438	2	G83350	hypothetical prote
220	6	4.4	443	2	T31644	probable carboxyl-
221	6	4.4	446	2	G75383	hypothetical prote
222	6	4.4	447	2	G83740	hypothetical prote
223	6	4.4	450	2	D83036	UDP-N-acetylglucos
224	6	4.4	452	2	S43175	nttc protein - Rho
225	6	4.4	453	2	A54175	regulatory protein
226	6	4.4	455	2	S54604	1-aminocyclopropan
227	6	4.4	457	2	S27257	glycosyltransferas
228	6	4.4	463	2	S36176	probable glucosylt
229	6	4.4	465	2	T00090	hypothetical prote
230	6	4.4	466	2	T22141	hypothetical prote
231	6	4.4	466	2	F84644	hypothetical prote
232	6	4.4	466	2	A64411	hypothetical prote
233	6	4.4	469	2	A64411	glycosyltransferas
234	6	4.4	476	2	T03747	leucine aminopepti
235	6	4.4	476	2	B82414	REP3 protein homol
236	6	4.4	476	2	S60381	d phosphogluconate d
237	6	4.4	480	1	JH0531	hypothetical prote
238	6	4.4	481	1	T28900	alanine transaminase
239	6	4.4	481	2	S70887	phosphomannomutase
240	6	4.4	483	2	T44335	hypothetical prote
241	6	4.4	483	2	T48119	hypothetical prote
242	6	4.4	486	2	B69680	pata-nitrobenzyl e
243	6	4.4	489	2	C71410	hypothetical prote
244	6	4.4	495	2	S50508	AMP1 protein - yea
245	6	4.4	500	2	S23243	hypothetical prote
246	6	4.4	503	2	T05272	fatty acid elongas
247	6	4.4	506	2		
248	6	4.4				

249	6	4.4	508	2	E71620	hypothetical prote	322	6	4.4	748	1	S08680	methionylmalonyl-CoA
250	6	4.4	508	2	T20757	hypothetical prote	323	6	4.4	750	1	A59145	methionylmalonyl-CoA
251	6	4.4	511	2	T51544	hypothetical prote	324	6	4.4	753	2	T32844	hypothetical prote
252	6	4.4	513	2	T45658	1-phosphatidylinos	325	6	4.4	756	2	G84866	hypothetical prote
253	6	4.4	520	2	T45765	hypothetical prote	326	6	4.4	757	2	D84175	zinc-transferrin
254	6	4.4	520	2	T49478	probable glutamate	327	6	4.4	760	2	F75530	ribonuclease - Dei
255	6	4.4	522	2	C96608	hypothetical prote	328	6	4.4	764	2	E84516	probable retroelem
256	6	4.4	523	2	D83631	probable sulfate t	329	6	4.4	767	2	T00360	hypothetical prote
257	6	4.4	526	2	A34896	adenylate cyclase-	330	6	4.4	768	2	F17350	probable protein-e
258	6	4.4	526	2	T48467	aspartyl aminopept	331	6	4.4	769	1	P1BP66	pi protein - phage
259	6	4.4	529	2	S44649	f42h10.7 protein -	332	6	4.4	771	2	T34376	hypothetical prote
260	6	4.4	531	1	S54098	1-phosphatidylinos	333	6	4.4	772	2	C75579	catalase - Deinoco
261	6	4.4	532	2	T06029	hypothetical prote	334	6	4.4	772	2	T02805	chloride channel p
262	6	4.4	534	2	S26877	groEL protein - re	335	6	4.4	782	2	T12134	hypothetical prote
263	6	4.4	535	2	T52098	probable nuclear t	336	6	4.4	794	2	S50687	hypothetical prote
264	6	4.4	537	2	A86154	hypothetical prote	337	6	4.4	794	2	F72202	hypothetical prote
265	6	4.4	538	2	B81376	probable membrane	338	6	4.4	798	2	S62791	probable lipoprote
266	6	4.4	540	2	E69861	ABC transporter (A	339	6	4.4	800	2	S53079	PER111 protein - Y
267	6	4.4	548	2	C75499	groEL protein - De	340	6	4.4	803	2	B84931	DNA topoisomerase
268	6	4.4	550	2	G86667	hypothetical prote	341	6	4.4	807	2	T32463	hypothetical prote
269	6	4.4	550	2	T29919	hypothetical prote	342	6	4.4	814	1	C40618	fibrral outer mem
270	6	4.4	553	2	H64494	hypothetical prote	343	6	4.4	821	1	S67087	hypothetical prote
271	6	4.4	565	2	G82443	conserved hypotet	344	6	4.4	822	2	H69547	molybdopterin oxid
272	6	4.4	569	2	T43531	probable potassium	345	6	4.4	822	2	T48742	ryanodine receptor
273	6	4.4	574	1	HMIIVB	hemagglutinin prec	346	6	4.4	827	1	A36895	endopeptidase Ia (
274	6	4.4	575	1	HMIIVB	hemagglutinin prec	347	6	4.4	827	1	S56404	virulence associat
275	6	4.4	575	1	S01862	hemagglutinin prec	348	6	4.4	827	1	C86114	probable enzyme va
276	6	4.4	576	2	S03300	hemagglutinin prec	349	6	4.4	837	2	T48407	hypothetical prote
277	6	4.4	578	2	S03299	hemagglutinin prec	350	6	4.4	837	2	JN0292	antigen 332 - mala
278	6	4.4	580	2	S03301	hemagglutinin prec	351	6	4.4	839	2	C84697	hypothetical prote
279	6	4.4	580	2	A82447	probable 5'-nucleo	352	6	4.4	844	2	T32608	hypothetical prote
280	6	4.4	581	2	T38501	hypothetical prote	353	6	4.4	856	2	H64552	endopeptidase Clp
281	6	4.4	583	1	HMIIVB	hemagglutinin prec	354	6	4.4	862	2	T05941	lipoxigenase (EC 1
282	6	4.4	583	1	HMIIVB	hemagglutinin prec	355	6	4.4	862	2	T40934	probable integral
283	6	4.4	584	1	HMIIVB	hemagglutinin prec	356	6	4.4	865	2	T11852	lipoxigenase (EC 1
284	6	4.4	585	1	HMIIVB	hemagglutinin prec	357	6	4.4	867	2	B96625	hypothetical prote
285	6	4.4	610	2	H71612	asparagine--tRNA l	358	6	4.4	874	2	B70945	hypothetical prote
286	6	4.4	614	2	A96716	probable fructokin	359	6	4.4	875	2	I59350	hypothetical prote
287	6	4.4	627	2	S46820	hypothetical prote	360	6	4.4	876	2	T05943	probable lipoxigen
288	6	4.4	628	1	A39262	transcription fact	361	6	4.4	876	2	I52907	importin beta chal
289	6	4.4	628	1	A33333	transcription fact	362	6	4.4	876	2	S66288	nuclear pore-targe
290	6	4.4	630	1	A46149	transcription fact	363	6	4.4	887	2	T20941	hypothetical prote
291	6	4.4	631	2	T13115	protein gp29 - pha	364	6	4.4	892	2	S76350	hypothetical prote
292	6	4.4	632	2	T38126	probable electron	365	6	4.4	902	2	S61144	glycogen phosphory
293	6	4.4	635	2	S57714	csfB protein - Cio	366	6	4.4	902	2	B84652	hypothetical prote
294	6	4.4	638	1	TVXLRF	protein kinase raf	367	6	4.4	906	2	A71438	probable resistanc
295	6	4.4	640	1	D83571	conserved hypotet	368	6	4.4	910	2	S07838	SEC15 protein - ye
296	6	4.4	644	2	C86747	topoisomerase IV s	369	6	4.4	949	2	E71940	translational initia
297	6	4.4	651	2	F64457	methionine--tRNA l	370	6	4.4	961	2	T01167	hypothetical prote
298	6	4.4	651	2	A86333	dnak-type molecula	371	6	4.4	966	1	PHPOAG	starch phosphoryla
299	6	4.4	652	2	D85044	hypothetical prote	372	6	4.4	969	2	T15446	hypothetical prote
300	6	4.4	662	2	D54078	methy1-accepting c	373	6	4.4	984	2	E70406	DMSO reductase cha
301	6	4.4	664	2	S66067	methionine--tRNA l	374	6	4.4	987	2	H86197	hypothetical prote
302	6	4.4	668	2	T15305	hypothetical prote	375	6	4.4	987	2	T40241	probable guanine n
303	6	4.4	672	2	T32557	hypothetical prote	376	6	4.4	997	2	S33754	glutamate receptor
304	6	4.4	676	2	A81349	probable ATP-depen	377	6	4.4	1000	2	I46521	fitin - rabbit (fr
305	6	4.4	677	2	G69895	formate dehydrogen	378	6	4.4	1013	2	T16244	hypothetical prote
306	6	4.4	684	2	F85075	hypothetical prote	379	6	4.4	1018	1	F73720	cyadherence acces
307	6	4.4	686	2	A71607	Mtn3/RAG1P-like p	380	6	4.4	1025	2	S50293	multidrug resistanc
308	6	4.4	696	2	S75626	hypothetical prote	381	6	4.4	1025	2	T18376	hypothetical prote
309	6	4.4	700	2	T43469	hypothetical prote	382	6	4.4	1029	2	H96658	hypothetical prote
310	6	4.4	704	2	T34034	hypothetical prote	383	6	4.4	1036	2	B69368	hypothetical prote
311	6	4.4	705	2	A41322	N-acetylmuramoyl-L	384	6	4.4	1096	2	T48512	hypothetical prote
312	6	4.4	706	2	A45990	junctional sarcopl	385	6	4.4	1120	2	T38431	DNA-directed RNA p
313	6	4.4	710	2	H72341	vachB protein - The	386	6	4.4	1132	2	T03844	telomerase catalyt
314	6	4.4	715	2	S70397	zona pellucida gly	387	6	4.4	1211	2	C71817	DNA polymerase III
315	6	4.4	720	2	T36293	probable serine/th	388	6	4.4	1211	2	D64702	DNA polymerase III
316	6	4.4	728	1	A35644	hepatocyte growth	389	6	4.4	1225	1	B64234	hypothetical prote
317	6	4.4	728	1	A60185	hepatocyte growth	390	6	4.4	1235	2	C69165	hypothetical prote
318	6	4.4	732	2	T08420	1-phosphatidylinos	391	6	4.4	1243	2	UC5615	membrane-associate
319	6	4.4	737	2	T31349	hypothetical prote	392	6	4.4	1262	2	T22523	hypothetical prote
320	6	4.4	737	2	T15615	hypothetical prote	393	6	4.4	1270	2	T26720	hypothetical prote
321	6	4.4	744	2	A70385	DNA gyrase A subun	394	6	4.4	1272	2	T49313	copia-type reverse

395	6	4.4	1274	2	D84485	probable retroelem
396	6	4.4	1276	2	T02711	probable calmoduli
397	6	4.4	1284	2	G83897	conserved hypothet
398	6	4.4	1300	2	T53799	CGI protein - huma
399	6	4.4	1320	2	F96614	probable copia-lyp
400	6	4.4	1352	2	F86246	hypothetical prote
401	6	4.4	1352	2	T47925	copia-type polypro
402	6	4.4	1354	2	S74244	serine/threonine-s
403	6	4.4	1354	2	S69211	serine/threonine-s
404	6	4.4	1356	2	S32763	kinectin 1 - huma
405	6	4.4	1369	2	T33338	hypothetical prote
406	6	4.4	1466	2	G84516	probable retroelem
407	6	4.4	1486	2	G64832	cell division prot
408	6	4.4	1486	2	E85618	hypothetical prote
409	6	4.4	1534	2	JH0228	cell division prot
410	6	4.4	1629	2	T06461	DNA-binding protei
411	6	4.4	1650	2	T18444	hypothetical prote
412	6	4.4	1742	2	S76110	hypothetical prote
413	6	4.4	1787	2	F84528	probable retroelem
414	6	4.4	1872	2	JC4976	plexin 3 precursor
415	6	4.4	1883	2	G82875	hypothetical prote
416	6	4.4	1888	2	T14273	zinc finger protei
417	6	4.4	1894	2	JC4980	plexin 1 precursor
418	6	4.4	1905	2	T53553	plexin - African c
419	6	4.4	1948	2	B69511	N conserved hypoch
420	6	4.4	1957	2	S68453	sodium channel pro
421	6	4.4	1968	1	S05697	myosin heavy chain
422	6	4.4	2172	2	T00936	probable ATP-depen
423	6	4.4	2206	2	G71611	hypothetical prote
424	6	4.4	2232	2	T34434	hypothetical prote
425	6	4.4	2331	2	T25410	hypothetical prote
426	6	4.4	2340	2	B71704	cell surface antiq
427	6	4.4	2485	1	H71621	serine/threonine-s
428	6	4.4	3079	1	RC8Y12	probable GTPase-ac
429	6	4.4	3488	2	T34418	hypothetical prote
430	6	4.4	3519	2	S43048	polyketide synthas
431	6	4.4	4558	2	C82199	RTX toxin RtxA Vcl
432	6	4.4	4589	2	T14914	dynamin beta heavy
433	6	4.4	4688	2	F82885	hypothetical prote
434	6	4.4	4667	2	S72269	ryanodine receptor
435	6	4.4	4699	2	A37113	ryanodine receptor
436	6	4.4	4981	2	T18489	hypothetical prote
437	6	4.4	6805	2	S20901	titin - rabbit (fr
438	6	4.4	26926	1	I38344	titin, cardiac mus
439	5	3.7	17	2	S20490	photosystem II chl
440	5	3.7	17	2	S66364	sodium-translocat
441	5	3.7	21	2	C49042	Ig heavy chain V r
442	5	3.7	21	2	B49042	Ig heavy chain V r
443	5	3.7	25	2	PH1715	Ig heavy chain V r
444	5	3.7	26	2	T14041	NADH dehydrogenase
445	5	3.7	26	2	T14221	NADH dehydrogenase
446	5	3.7	26	2	F49164	chromogranin-B - r
447	5	3.7	32	2	S58413	phospholipase A2 (
448	5	3.7	32	2	H82416	hypothetical prote
449	5	3.7	33	2	S22602	ribosomal protein
450	5	3.7	38	2	T19769	hypothetical prote
451	5	3.7	39	2	G83716	hypothetical prote
452	5	3.7	41	2	I44530	T-cell receptor al
453	5	3.7	42	2	S06812	myosin heavy chain
454	5	3.7	42	2	S06813	Ig heavy chain V r
455	5	3.7	44	2	PL0091	Ig heavy chain V r
456	5	3.7	44	2	E37286	olfactory receptor
457	5	3.7	45	2	JC5274	thymosin beta - hu
458	5	3.7	45	2	PL0094	Ig heavy chain V r
459	5	3.7	48	2	S61469	p83/100 protein -
460	5	3.7	48	2	S61472	p83/100 protein -
461	5	3.7	49	1	T0B01	thymopoietin I - b
462	5	3.7	49	1	T0B02	thymopoietin II -
463	5	3.7	49	1	T0B03	thymopoietin III -
464	5	3.7	52	1	RUDVEG	rubredoxin [valida
465	5	3.7	52	2	A71002	hypothetical prote
466	5	3.7	53	2	B25507	proteinase inhibit
467	5	3.7	54	2	F82711	50S ribosomal prot
468	5	3.7	54	2	E45681	hypothetical 5.9K
469	5	3.7	55	1	BCGR	spermatid transiti
470	5	3.7	55	1	BCGR	hypothetical prote
471	5	3.7	56	2	B86805	hypothetical prote
472	5	3.7	56	2	H81353	T-cell receptor al
473	5	3.7	57	2	D49056	DNA topoisomerase
474	5	3.7	58	2	A35416	neurotoxin V-5 - b
475	5	3.7	59	2	C23727	hypothetical prote
476	5	3.7	59	2	A72392	small hydrophobic
477	5	3.7	59	2	D81363	H+-transporting AT
478	5	3.7	59	2	C36493	hypothetical prote
479	5	3.7	61	2	B34888	hypothetical prote
480	5	3.7	61	2	S42858	hypothetical prote
481	5	3.7	62	2	JQ2194	hypothetical 6.7K
482	5	3.7	64	2	PC4361	pepsinogen C-1 - h
483	5	3.7	65	2	T09827	polygalacturonase
484	5	3.7	66	2	T07880	protein kinase (EC
485	5	3.7	67	2	G69058	hypothetical prote
486	5	3.7	69	2	A41903	recombinase homolo
487	5	3.7	69	2	E86644	hypothetical prote
488	5	3.7	69	2	T45696	hypothetical prote
489	5	3.7	70	2	T06525	cytochrome P450 ho
490	5	3.7	70	2	T12789	bacteriocin homolo
491	5	3.7	71	1	IHRC	high potential iro
492	5	3.7	74	2	S68269	Y-box binding prot
493	5	3.7	75	2	A25155	Ig heavy chain V r
494	5	3.7	75	2	C70523	hypothetical prote
495	5	3.7	76	1	S76753	hypothetical prote
496	5	3.7	76	1	S11704	aminoglycoside 3''
497	5	3.7	76	2	F70317	RNA polymerase ome
498	5	3.7	78	2	A82011	probable integral
499	5	3.7	78	2	D72764	probable ferredoxi
500	5	3.7	79	2	B83230	probable acyl carr
501	5	3.7	79	2	G64375	hypothetical prote
502	5	3.7	80	2	S25050	Ig heavy chain V r
503	5	3.7	80	2	E64307	ferredoxin - Metha
504	5	3.7	81	2	C86119	hypothetical prote
505	5	3.7	81	2	D65233	hypothetical 9.6 k
506	5	3.7	81	2	B84149	hypothetical prote
507	5	3.7	82	2	I51133	MHC class II beta
508	5	3.7	82	2	S22306	hypothetical prote
509	5	3.7	83	2	I46058	caldesmon - bovine
510	5	3.7	84	2	PH1487	Ig heavy chain V r
511	5	3.7	85	2	T12867	hypothetical prote
512	5	3.7	86	2	T03624	reverse transcript
513	5	3.7	86	2	H83457	hypothetical prote
514	5	3.7	87	2	T03716	reverse transcript
515	5	3.7	87	2	T06281	reverse transcript
516	5	3.7	87	2	B85510	hypothetical 10K p
517	5	3.7	87	2	T01264	hypothetical prote
518	5	3.7	87	2	T23257	hypothetical prote
519	5	3.7	87	2	S27275	GTP-binding regula
520	5	3.7	88	2	S77429	glutaredoxin 3 - S
521	5	3.7	88	2	E25155	Ig heavy chain V r
522	5	3.7	88	2	G70331	anti sigma factor
523	5	3.7	89	2	G81106	DNA-binding protei
524	5	3.7	89	2	T14589	reverse transcript
525	5	3.7	89	2	D64414	hypothetical prote
526	5	3.7	89	2	B32227	hypothetical prote
527	5	3.7	89	2	T44502	meRE protein homol
528	5	3.7	89	2	T25923	hypothetical prote
529	5	3.7	91	1	R3MX10	ribosomal protein
530	5	3.7	91	1	PC4194	phospholipase D (E
531	5	3.7	92	1	Z1BPC2	regulatory proteins
532	5	3.7	92	1	JN0906	cystatin proteinas
533	5	3.7	92	2	T03623	reverse transcript
534	5	3.7	92	2	S76032	hypothetical prote
535	5	3.7	92	2	S56289	heterocyst diftere
536	5	3.7	93	2	C24672	Ig heavy chain V r
537	5	3.7	93	2	A25343	nonhistone chromos
538	5	3.7	93	2	S13717	histone-like prote
539	5	3.7	93	2	F86063	hypothetical prote
540	5	3.7	93	2	S46658	peptidylprolyl iso

541	5	3.7	93	2	E69510	proteinase inhibit
542	5	3.7	94	2	G32513	Ig heavy chain V r
543	5	3.7	94	2	JC1164	hypothetical 10.3K
544	5	3.7	94	2	C59094	hypothetical prote
545	5	3.7	94	2	D75066	lsu ribosomal prot
546	5	3.7	95	2	S12888	DNA-binding protei
547	5	3.7	96	1	FEXCAL	ferredoxin [2Fe-2S
548	5	3.7	96	2	S16215	xyulokinas (EC 2
549	5	3.7	96	2	JC5945	regulatory protein
550	5	3.7	96	2	S38916	hypothetical prote
551	5	3.7	96	2	S78713	protein YDR322c-a
552	5	3.7	97	1	FEXCT	ferredoxin [2Fe-2S
553	5	3.7	97	2	T15891	hypothetical prote
554	5	3.7	98	1	KRGLBS	keratin, feather -
555	5	3.7	98	2	JX0083	ferredoxin [2Fe-2S
556	5	3.7	98	2	S22432	hydroxymethylgluta
557	5	3.7	98	2	T42909	hypothetical prote
558	5	3.7	98	2	T12887	hypothetical prote
559	5	3.7	99	2	B44866	major metazoite su
560	5	3.7	99	2	A44866	major metazoite su
561	5	3.7	99	2	A42196	preprotein translo
562	5	3.7	99	2	D75129	hypothetical prote
563	5	3.7	99	2	T21919	hypothetical prote
564	5	3.7	100	2	G84990	50S ribosomal prot
565	5	3.7	100	2	P00818	expressed sequence
566	5	3.7	100	2	C44866	major metazoite su
567	5	3.7	100	2	H85952	hypothetical prote
568	5	3.7	100	2	H65080	hypothetical prote
569	5	3.7	101	1	I64075	urease (EC 3.5.1.5
570	5	3.7	101	2	S26311	Ig heavy chain V r
571	5	3.7	101	2	G70770	hypothetical prote
572	5	3.7	101	2	S29093	SM3 protein - yea
573	5	3.7	101	2	G96664	hypothetical prote
574	5	3.7	101	2	E69442	conserved hypotet
575	5	3.7	102	1	CCDV3D	cytochrome c3 - De
576	5	3.7	102	2	S54825	glutaredoxin - cas
577	5	3.7	102	2	PH1490	Ig heavy chain V r
578	5	3.7	102	2	PH1491	Ig heavy chain V r
579	5	3.7	102	2	F75077	hypothetical prote
580	5	3.7	103	2	S28823	transcription fact
581	5	3.7	104	1	CCCZ	cytochrome c - chi
582	5	3.7	104	1	CCMOR	cytochrome c - rhe
583	5	3.7	104	1	CCMKP	cytochrome C - spi
584	5	3.7	104	2	G86739	50S ribosomal prot
585	5	3.7	104	2	S72391	hypothetical prote
586	5	3.7	104	2	B71180	hypothetical prote
587	5	3.7	104	2	T13628	hypothetical prote
588	5	3.7	104	2	T13323	hypothetical prote
589	5	3.7	104	2	T17947	hypothetical prote
590	5	3.7	104	2	T36976	probable transposa
591	5	3.7	105	1	CCHU	cytochrome c [vali
592	5	3.7	105	2	H69949	transcription regu
593	5	3.7	105	2	JQ2140	hypothetical 12.2K
594	5	3.7	105	2	B47119	spore coat protein
595	5	3.7	105	2	C81394	hypothetical prote
596	5	3.7	105	2	H81293	hypothetical prote
597	5	3.7	105	2	E69326	hypothetical prote
598	5	3.7	106	2	C69772	thioredoxin homolo
599	5	3.7	106	2	J50484	ribonuclease FI (E
600	5	3.7	106	2	S13027	cysteine proteinas
601	5	3.7	106	2	S59639	Ig heavy chain V r
602	5	3.7	106	2	S26464	Ig heavy chain V r
603	5	3.7	106	2	S25036	Ig heavy chain V r
604	5	3.7	106	2	H82094	bola protein WC229
605	5	3.7	106	2	F71075	hypothetical prote
606	5	3.7	106	2	H84333	hypothetical prote
607	5	3.7	106	2	B64001	hypothetical prote
608	5	3.7	106	2	S45762	hypothetical prote
609	5	3.7	106	2	S32032	Sp17 protein precu
610	5	3.7	107	2	A27646	Ig heavy chain V r
611	5	3.7	107	2	PI0240	Ig heavy chain V r
612	5	3.7	107	2	PI0243	Ig heavy chain V r
613	5	3.7	107	2	PI0241	Ig heavy chain V r
<hr/>						
614	5	3.7	107	2	JC1127	major allergen cha
615	5	3.7	107	2	T47876	hypothetical prote
616	5	3.7	107	2	T10041	hypothetical prote
617	5	3.7	107	2	T42903	hypothetical prote
618	5	3.7	107	2	T42918	hypothetical prote
619	5	3.7	108	2	PI0248	Ig heavy chain V r
620	5	3.7	108	2	S31953	Ig heavy chain V r
621	5	3.7	108	2	S31954	penicillin-binding
622	5	3.7	108	2	S77095	hypothetical prote
623	5	3.7	108	2	C64510	hypothetical prote
624	5	3.7	108	2	T26681	hypothetical prote
625	5	3.7	109	1	L1HWVA	Ig lambda chain V-
626	5	3.7	109	1	R3MX17	ribosomal protein
627	5	3.7	109	2	S27053	thioredoxin - Emer
628	5	3.7	109	2	S25038	Ig heavy chain V r
629	5	3.7	109	2	B64145	hypothetical prote
630	5	3.7	109	2	D71209	probable ribosomal
631	5	3.7	109	2	C56413	major allergen Fel
632	5	3.7	109	2	B64492	hypothetical prote
633	5	3.7	109	2	E84202	ferredoxin [import
634	5	3.7	110	1	R5BYA1	acidic ribosomal p
635	5	3.7	110	2	A45938	transcription fact
636	5	3.7	110	2	S57412	Ig lambda chain V-
637	5	3.7	110	2	A32189	Ig heavy chain V r
638	5	3.7	110	2	P00494	glycoprotein I - C
639	5	3.7	110	2	F69760	hypothetical prote
640	5	3.7	110	2	C71160	hypothetical prote
641	5	3.7	110	2	S74013	hypothetical prote
642	5	3.7	111	1	MEMS76	Ig heavy chain V-I
643	5	3.7	111	2	S25052	Ig heavy chain V r
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650	5	3.7	111	2	S25051	Ig heavy chain V r
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652	5	3.7	111	2	S25033	Ig heavy chain V r
653	5	3.7	111	2	S25045	Ig heavy chain V r
654	5	3.7	111	2	S25045	Ig heavy chain V r
655	5	3.7	111	2	S25034	Ig heavy chain V r
656	5	3.7	111	2	S25024	Ig heavy chain V r
657	5	3.7	111	2	G70772	hypothetical prote
658	5	3.7	112	1	R5FE2E	acidic ribosomal p
659	5	3.7	112	2	S09957	Ig heavy chain V-D
660	5	3.7	112	2	T38889	probable acyl carr
661	5	3.7	112	2	H69447	hypothetical prote
662	5	3.7	112	2	S58139	gene 9 protein - P
663	5	3.7	112	2	B48941	pediocin productio
664	5	3.7	112	2	B86441	hypothetical prote
665	5	3.7	112	2	H70878	probable regulator
666	5	3.7	113	2	B36259	Ig heavy chain V r
667	5	3.7	113	2	S25041	Ig heavy chain V r
668	5	3.7	113	2	S25044	Ig heavy chain V r
669	5	3.7	113	2	D71205	hypothetical prote
670	5	3.7	113	2	I40399	flagellar protein
671	5	3.7	113	2	T19198	hypothetical prote
672	5	3.7	114	2	T01262	Ig heavy chain V r
673	5	3.7	114	2	S46377	Ig kappa chain V-J
674	5	3.7	114	2	S11105	Ig heavy chain V r
675	5	3.7	114	2	T08325	hypothetical prote
676	5	3.7	114	2	JC6077	p13 protein - Leuc
677	5	3.7	114	2	T20095	nitrophenyl phosph
678	5	3.7	114	4	A47271	Ig heavy chain V r
679	5	3.7	115	2	S19965	Ig heavy chain V r
680	5	3.7	115	2	S19968	Ig heavy chain V r
681	5	3.7	115	2	S38714	Ig heavy chain V r
682	5	3.7	115	2	A54378	Ig heavy chain V r
683	5	3.7	115	2	A56700	Ig heavy chain (an
684	5	3.7	115	2	S03482	Ig heavy chain V-D
685	5	3.7	115	2	S77491	ribosomal protein
686	5	3.7	115	2	A83776	hypothetical prote

833	5	3.7	132	2	T03397	hypothetical prote	906	5	3.7	141	2	T09581	probable high mobi
834	5	3.7	133	2	PC1155	Ig heavy chain pre	907	5	3.7	142	2	C32394	succinate dehydrog
835	5	3.7	133	2	B81449	hypothetical prote	908	5	3.7	142	2	S71361	actin-binding prot
836	5	3.7	133	2	S69803	hypothetical prote	909	5	3.7	142	2	G64952	hypothetical 17.1
837	5	3.7	134	2	S73181	H+-transporting AT	910	5	3.7	142	2	H85802	probable regulator
838	5	3.7	134	2	E57233	complexin II - hum	911	5	3.7	142	2	D75134	hypothetical prote
839	5	3.7	134	2	D57233	complexin II - mou	912	5	3.7	142	2	D72040	conserved hypotet
840	5	3.7	134	2	JC4226	synaphin - bovine	913	5	3.7	142	2	C86583	Ct635 hypothetical
841	5	3.7	134	2	S66294	921-S protein - mo	914	5	3.7	142	2	E84369	histidine triad pr
842	5	3.7	134	2	A57233	complexin I - rat	915	5	3.7	142	2	S46445	YMF46 protein - Ac
843	5	3.7	134	2	C57233	complexin II - rat	916	5	3.7	142	2	T34136	hypothetical prote
844	5	3.7	134	2	A82455	hypothetical prote	917	5	3.7	143	1	RGMX15	ribosomal protein
845	5	3.7	134	2	G82477	hypothetical prote	918	5	3.7	143	2	B32384	succinate dehydrog
846	5	3.7	134	2	E70251	hypothetical prote	919	5	3.7	143	2	D69083	hypothetical prote
847	5	3.7	134	2	E75582	hypothetical prote	920	5	3.7	143	2	F86736	general stress pro
848	5	3.7	134	2	T12219	glutaredoxin I - c	921	5	3.7	143	2	T31273	hypothetical prote
849	5	3.7	135	1	PWLVE	H+-transporting AT	922	5	3.7	144	2	S23658	superoxide dismuta
850	5	3.7	135	2	PL0100	Ig heavy chain pre	923	5	3.7	144	2	B30502	Ig heavy chain V r
851	5	3.7	135	2	S31913	Ig gamma-2A chain	924	5	3.7	144	2	T43374	ribosomal protein
852	5	3.7	135	2	I56326	fatty acid binding	925	5	3.7	144	2	G11959	neutrophil-activat
853	5	3.7	136	1	HVMSB1	Ig heavy chain pre	926	5	3.7	144	2	C64550	neutrophil activat
854	5	3.7	136	1	R5EC16	ribosomal protein	927	5	3.7	144	2	B72214	hypothetical prote
855	5	3.7	136	2	JL0077	Ig heavy chain pre	928	5	3.7	144	2	C70455	hypothetical prote
856	5	3.7	136	2	PL0208	Ig heavy chain pre	929	5	3.7	144	2	A69399	hypothetical prote
857	5	3.7	136	2	B47159	Ig heavy chain V r	930	5	3.7	144	2	C83974	hypothetical prote
858	5	3.7	136	2	S13791	Ig heavy chain V r	931	5	3.7	144	2	E86618	hypothetical prote
859	5	3.7	136	2	T30159	hypothetical prote	932	5	3.7	144	2	A84168	hypothetical prote
860	5	3.7	136	2	C64093	ribosomal protein	933	5	3.7	144	2	T08666	ribosomal protein
861	5	3.7	136	2	F85996	50S ribosomal subu	934	5	3.7	145	1	R5RT26	transcription regu
862	5	3.7	136	2	G82058	ribosomal protein	935	5	3.7	145	1	G69867	superoxide dismuta
863	5	3.7	136	2	S73520	MG441 homolog E09-	936	5	3.7	145	2	S54794	Ig heavy chain pre
864	5	3.7	136	2	T22240	hypothetical prote	937	5	3.7	145	2	S03844	ribosomal protein
865	5	3.7	136	2	T22797	hypothetical prote	938	5	3.7	145	2	S33713	ribosomal protein
866	5	3.7	137	1	G2M543	Ig heavy chain pre	939	5	3.7	145	2	S48864	hypothetical prote
867	5	3.7	137	1	AVMS35	Ig heavy chain pre	940	5	3.7	145	2	T33961	hypothetical prote
868	5	3.7	137	2	H32513	Ig heavy chain pre	941	5	3.7	145	2	T13550	hypothetical prote
869	5	3.7	137	2	B64208	hypothetical prote	942	5	3.7	145	2	H84174	hypothetical prote
870	5	3.7	137	2	B70123	conserved hypotet	943	5	3.7	145	2	B72724	hypothetical prote
871	5	3.7	137	2	G71551	hypothetical prote	944	5	3.7	145	2	S37043	Salt protein precu
872	5	3.7	137	2	T22872	hypothetical prote	945	5	3.7	145	2	S19929	microtubulin - associ
873	5	3.7	137	2	S54618	hypothetical prote	946	5	3.7	146	1	S24311	flavodoxin - Deesul
874	5	3.7	138	2	G81231	50S ribosomal prot	947	5	3.7	146	1	R3MX7	ribosomal protein
875	5	3.7	138	2	S24103	envelope protein -	948	5	3.7	146	2	B64246	ribosomal protein
876	5	3.7	138	2	T02653	ascorbic acid- and	949	5	3.7	146	2	H72167	A35R protein - var
877	5	3.7	138	2	G82116	flagellar motor sw	950	5	3.7	146	2	S73456	DNA-directed RNA p
878	5	3.7	138	2	S36115	interferon - Japan	951	5	3.7	146	2	G70020	hypothetical prote
879	5	3.7	139	1	MEMS18	Ig heavy chain pre	952	5	3.7	146	4	S33905	Ig heavy chain pre
880	5	3.7	139	2	A61089	beta-crystallin B3	953	5	3.7	147	2	F84153	ribosomal protein
881	5	3.7	139	2	H64302	conserved hypotet	954	5	3.7	147	2	D75132	probable hydrogena
882	5	3.7	139	2	F82863	conserved hypotet	955	5	3.7	147	2	F71089	probable hydrogena
883	5	3.7	139	2	C83807	hypothetical prote	956	5	3.7	147	2	A69933	hypothetical prote
884	5	3.7	140	2	PH1482	Ig heavy chain V r	957	5	3.7	147	2	G70795	hypothetical prote
885	5	3.7	140	2	PH1483	Ig heavy chain V r	958	5	3.7	147	2	F83801	chordate mutase
886	5	3.7	140	2	PH1484	Ig heavy chain V r	959	5	3.7	147	2	H82172	heat shock protein
887	5	3.7	140	2	PH1488	Ig heavy chain V r	960	5	3.7	147	2	E69780	conserved hypotet
888	5	3.7	140	2	PH1489	Ig heavy chain V r	961	5	3.7	148	1	T12787	probable protein-d
889	5	3.7	140	2	PH1498	Ig heavy chain V r	962	5	3.7	148	2	A57569	tau-star protein -
890	5	3.7	140	2	S06816	Ig heavy chain pre	963	5	3.7	148	2	C82544	limbrial protein x
891	5	3.7	140	2	A36194	Ig heavy chain V r	964	5	3.7	148	2	T33812	hypothetical prote
892	5	3.7	140	2	B69496	small heat shock p	965	5	3.7	148	2	A72785	hypothetical prote
893	5	3.7	140	2	S31628	MA28L protein - my	966	5	3.7	148	2	C75212	hypothetical prote
894	5	3.7	140	2	H69405	hypothetical prote	967	5	3.7	148	2	T32508	hypothetical prote
895	5	3.7	140	2	T28576	6R protein - vario	968	5	3.7	149	2	H70441	ribosomal protein
896	5	3.7	140	2	H36851	RNA-binding ribonu	969	5	3.7	149	2	S36992	transposase (clone
897	5	3.7	140	2	E70632	hypothetical prote	970	5	3.7	149	2	B37169	TUD4 protein precu
898	5	3.7	141	2	JL0076	endonuclease V-Lik	971	5	3.7	149	2	S39556	high mobility grou
899	5	3.7	141	2	A39276	Ig heavy chain pre	972	5	3.7	149	2	G64414	hypothetical prote
900	5	3.7	141	2	S08118	histone H2A.VD - f	973	5	3.7	149	2	A54503	51k merozoit surf
901	5	3.7	141	2	S75127	hypothetical prote	974	5	3.7	150	2	H86646	deoxyuridine 5'-tr
902	5	3.7	141	2	S74873	hypothetical prote	975	5	3.7	150	2	H86194	hypothetical prote
903	5	3.7	141	2	S77513	hypothetical prote	976	5	3.7	150	2	B26368	protein-serine kin
904	5	3.7	141	2	E72781	hypothetical prote	977	5	3.7	150	2	F59105	hypothetical prote
905	5	3.7	141	2	E72781	hypothetical prote	978	5	3.7	151	2	S77475	ribosomal protein

979 5 3.7 151 2 A69227
 980 5 3.7 151 2 A35735
 981 5 3.7 151 2 C68352
 982 5 3.7 152 1 C69202
 983 5 3.7 152 2 B64369
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 988 5 3.7 153 2 S54841
 989 5 3.7 153 2 B60891
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 996 5 3.7 154 2 A05187
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 999 5 3.7 154 2 S39729
 1000 5 3.7 154 2 T03503

ALIGNMENTS

hypothetical prote
 regulatory protein
 protein T26F17.12
 conserved hypotet
 hypothetical prote
 hypothetical prote
 hypothetical prote
 hypothetical prote
 formate hydrogenly
 peptidylprolyl iso
 pilin - Dichelobac
 hypothetical prote
 hypothetical prote
 hypothetical prote
 probable bacteriof
 bacterioferritin A
 hypothetical prote
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 Skp1-like protein
 ywea protein - Bac
 conserved hypotet

RESULT 1
 PRSAK
 staphylokinase - phage S phi-C
 C:Species: phage S phi-C
 A:Note: host Staphylococcus aureus
 C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 28-May-1999
 C:Accession: A00995
 R:Sako, T.; Tsuchida, N.
 Nucleic Acids Res. 11, 7679-7693, 1983
 A:Title: Nucleotide sequence of the staphylokinase gene from Staphylococcus aureus.
 A:Reference number: A00995; MUID:84069795
 A:Accession: A00995
 A:Molecule type: DNA
 A:Residues: 1-163 <SAK>
 A:Cross-references: GB:X00127; NID:947425; PIDN:CAA24957.1; PID:9758303
 C:Comment: Although it has no intrinsic proteolytic activity, this secreted protein is a
 ructure of plasminogen is thought to expose the plasmin active site.
 C:Comment: The designation of staphylokinase as synonymous with Staphylococcal aureus ne
 C:Genetics:
 A:Gene: sak
 A:Superfamily: phage S phi-C staphylokinase
 C:Keywords: plasminogen activator

Query Match 75.0%; Score 102; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 7.1e-99;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 35 KGNELISPHYVEPIKPGTTLTKKEIEYVEMALDATAKERRVVELDPSAKIEVYTDK 94
 Db 62 KGNELISPHYVEPIKPGTTLTKKEIEYVEMALDATAKERRVVELDPSAKIEVYTDK 121
 Oy 95 NKKKEETKSPITTEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136
 Db 122 NKKKEETKSPITTEKGFVVPDLSEHIKNPGFNLTIKVIEKK 163

RESULT 2
 S02330
 staphylokinase - phage P42D
 C:Species: phage P42D
 A:Note: host Staphylococcus aureus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-Aug-1999
 C:Accession: S02330; S45654
 R:Behnke, D.; Gerlach, D.
 Mol. Gen. Genet. 210, 528-534, 1987

A:Title: Cloning and expression in Escherichia coli, Bacillus subtilis, and Streptoco
 A:Reference number: S02330; MUID:88121731
 A:Accession: S02330
 A:Molecule type: DNA
 A:Residues: 1-163 <BEH>
 A:Cross-references: EMBL:X06603; NID:946676; PIDN:CAA29822.1; PID:9758275
 R:Case, A.; Birch-Hirschfeld, E.; Guehrs, K.H.; Hartmann, M.; Vetterman, S.; Damaschu
 Eur. J. Biochem. 223, 303-308, 1994
 A:Title: The thermostability of natural variants of bacterial plasminogen-activator S
 A:Reference number: S45654; MUID:94307274
 A:Accession: S45654
 A:Molecule type: protein
 A:Residues: 28-163 <GAS>
 C:Genetics:
 A:Gene: sak
 C:Superfamily: phage S phi-C staphylokinase

Query Match 68.4%; Score 93; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.8e-89;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 44 YVEPIKPGTTLTKKEIEYVEMALDATAKERRVVELDPSAKIEVYTDK 103
 Db 71 YVEPIKPGTTLTKKEIEYVEMALDATAKERRVVELDPSAKIEVYTDK 130
 Oy 104 FPIITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 136
 Db 131 FPIITEKGFVVPDLSEHIKNPGFNLTIKVIEKK 163

RESULT 3
 A72218
 gufa protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: A72218
 R:Nejgon, K.E.; Clayton, R.A.; Gill, S.R.; Gwyn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: A72218
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <ARN>
 A:Cross-references: GB:AE001812; GB:AE000512; NID:94982302; PIDN:AAD36803.1; PID:9498
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1738
 C:Superfamily: gufa protein

Query Match 5.9%; Score 8; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 34 SKGNELLS 41
 Db 219 SKGNELLS 226

RESULT 4
 C69044
 hypothetical protein MTH1333 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: C69044
 R:Smith, D.R.; Doucet-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
 Qi, S.; Spadafora, R.; Viscare, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani,
 Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcn
A:Reference number: A69000; MUID:98037514
A:Accession: C69044
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-56 <MTH>
A:Cross-references: GB:AE000897; GB:AE000666; NID:92622439; PIDN:AB85811.1; PID:9262244
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1333

Query Match 5.1%; Score 7; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 TTITREK 59
|||||||
Db 16 TTITREK 22

RESULT 5
I46953
CGM-gated retinal photoreceptor channel - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 13-Aug-1999
C:Accession: I46953
R:Hundal, S.P.; DiFrancesco, D.; Mangoni, M.; Brammar, W.J.; Conley, E.C.
Biochem. Soc. Trans. 21, 119S, 1993.
A:Title: An isoform of the CGM-gated retinal photoreceptor channel gene expressed in th
A:Reference number: I46953; MUID:93365767
A:Accession: I46953
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-90 <HUV>
A:Cross-references: GB:S65218; NID:9410551; PIDN:AB27924.1; PID:9410552
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-

Query Match 5.1%; Score 7; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 KKEETK 102
|||||||
Db 6 KKEETK 12

RESULT 6
P00629
coat protein - tulip top-breaking virus (fragment)
C:Species: tulip top-breaking virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: P00629
R:Decker, E.L.; Derks, A.F.L.M.; Asjes, C.J.; Lemmers, M.E.C.; Bol, J.F.; Langeveld, S.A.
J. Gen. Virol. 74, 881-887, 1993
A:Title: Characterization of polynucleosides from tulip and lily which cause flower-breaking
A:Reference number: P00628; MUID:93260402
A:Accession: P00629
A:Molecule type: RNA
A:Residues: 1-92 <DEK>
A:Cross-references: GB:S60806; NID:9385510; PIDN:AB26636.1; PID:9385511
C:Superfamily: tobacco etch virus genome polypeptide
C:Keywords: coat protein

Query Match 5.1%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 VEPPIKP 51
|||||||
Db 18 VEPPIKP 24

RESULT 7
C84026
ribosomal protein L21 (BU20) rplU [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: C84026
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: C84026
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: GB:AP001517; GB:BA000004; NID:910175500; PIDN:BA06730.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: rplU
C:Superfamily: Escherichia coli ribosomal protein L21

Query Match 5.1%; Score 7; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 129 TKVIEK 135
|||||||
Db 93 TKVIEK 99

RESULT 8
D83704
transposase (14) BH0436 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: D83704
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: D83704
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <STO>
A:Cross-references: GB:AP001508; GB:BA000004; NID:910172890; PIDN:BA04155.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0436

Query Match 5.1%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 DSKGNEL 39
|||||||
Db 80 DSKGNEL 86

RESULT 9
F71501
hypothetical protein CT548 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: E71501
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71570; MUID:99000809
A:Accession: E71501
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-194 <ARN>
A:Cross-references: GB:AE001335; GB:AE001273; NID:g13328980; PIDN:AAC68150.1; PID:g3332898
A:Experimental source: serotype D, strain UW-3/CX
C:Genetics:
A:Gene: CTS48

Query Match 5.1%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 LSPHYE 46
Db 25 LSPHYE 31

RESULT 10

tryptophan synthase alpha chain [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84190
R:Ng, W.V.; Kennedy, S.P.; Mahaitas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leihauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jadhav, K.H.; Alam, M.; Freitas, F.; Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: D84190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <STO>
A:Cross-references: GB:AE004437; NID:g10579936; PIDN:AG18888.1; GSPDB:GN00138
C:Genetics:
A:Gene: trpA

Query Match 5.1%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GFVPDL 116
Db 51 GFVPDL 57

RESULT 11

hypothetical protein Y6E2A.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27336
R:Matthews, L.
A:Submitted to the EMBL Data Library, January 1998
A:Reference number: Z20347
A:Accession: T27336
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-219 <ML>
A:Cross-references: EMBL:AL021175; PIDN:CA15969.1; GSPDB:GN00023; CESP:Y6E2A.8
A:Experimental source: clone Y6E2A
C:Genetics:
A:Gene: CESP:Y6E2A.8
A:Map position: 5

Query Match 5.1%; Score 7; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 93 DKNKKE 99

Db 126 DKNKKE 132

RESULT 12

tryptophan synthase (EC 4.2.1.20) alpha chain [validated] - Haloferax volcanii (strain A36044)
C:Species: Haloferax volcanii
C>Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 26-May-2000
C:Accession: A36044
R:Ham, W.L.; Cohen, A.; Tsoulfas, D.; Doolittle, W.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 6614-6618, 1990
A:Title: Genes for tryptophan biosynthesis in the archaeobacterium Haloferax volcanii.
A:Reference number: A36044; MUID:90370836
A:Accession: A36044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <LAN>
A:Cross-references: GB:M36177; NID:g149041; PIDN:AA72864.1; PID:g149044
C:Genetics:
A:Gene: trpA
C:Function:
A:Description: EC 4.2.1.20 [validated; MUID:90370836]
C:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha homol
C:Keywords: carbon-oxygen lyase; hydro-lyase
F:12-240/Domain: tryptophan synthase alpha chain homology <TRPA>
F:43/Active site: Glu #status predicted

Query Match 5.1%; Score 7; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GFVPDL 116
Db 120 GFVPDL 126

RESULT 13

coat protein - turnip mosaic virus (strain UK1) (fragment)
C:Species: turnip mosaic virus, TURN
A:Variety: strain UK1
C>Date: 20-Feb-1995 #sequence_revision 26-Apr-1996 #text_change 17-Nov-2000
C:Accession: S21499
R:Lehmann, P.; Kozubek, E.; Ostrowka, K.; Walsh, J.; Greenland, A.
A:Submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence of the coat protein gene of Turnip mosaic virus tr
A:Reference number: S21499
A:Accession: S21499
A:Molecule type: DNA
A:Residues: 1-288 <LEH>
A:Cross-references: EMBL:X65978
A:Experimental source: strain UK1
C:Superfamily: tobacco etch virus genome polypeptide
C:Keywords: coat protein

Query Match 5.1%; Score 7; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 VEPPIK 51
Db 162 VEPPIK 168

RESULT 14

polyprotein - turnip mosaic virus (strain cgs) (fragment)
N:Contains: coat protein
C:Species: turnip mosaic virus, TURN
A:Variety: strain cgs

C;Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 17-Nov-2000
 C;Accession: S51329
 R;Choi, G.S.; Choi, J.K.
 A:Submitted to the EMBL Data Library, January 1995
 A:Description: Nucleotide sequence of coat protein gene of turnip mosaic virus (cgs strain)
 A:Reference number: S51329
 A;Accession: S51329
 A;Molecule type: genomic RNA
 A;Residues: 1-288 <CHO>
 A;Cross-references: EMBL:X83968; NID:g1552715; PIDN:CAA58802.1; PID:g634105
 A;Experimental source: strain cgs
 C;Superfamily: tobacco etch virus genome polyprotein
 C;Keywords: coat protein; polyprotein
 F;1-288/Product: coat protein #status predicted <MAT>

Query Match 5.1%; Score 7; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 VEPPIKP 51
 |||||
 Db 162 VEPPIKP 168

RESULT 15
 A83746
 transposase (16) BH0769 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C;Accession: A83746
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20263314
 A;Accession: A83746
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-311 <STO>
 A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04488.1; GSPDB:GN00
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH0769

Query Match 5.1%; Score 7; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 DSKGNEL 39
 |||||
 Db 262 DSKGNEL 268

Search completed: April 22, 2002, 10:46:10
 Job time: 130 sec

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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:45:45 ; Search time 12.01 Seconds

(without alignments)
415.189 Million cell updates/sec

Title: US-09-601-490-1

Perfect score: 136

Sequence: 1 SSSFDKGGKKKKGDASYEP.....SEHIKNPGFNLITRVIEKK 136

Scoring table: OLIGO

Searched: 100059 segs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	75.0	163	1	SAK_STAU
2	93	68.4	163	1	SAK_BP42
3	7	5.1	204	1	TRPA_HA1N1
4	7	5.1	231	1	CTRA_CAUCR
5	7	5.1	277	1	TRPA_HA1VO
6	7	5.1	334	1	TRXB_NEUCR
7	7	5.1	722	1	PBP1_YEAST
8	7	5.1	944	1	IF2_HELPY
9	7	5.1	1034	1	POL_HV2CA
10	7	5.1	1035	1	POL_HV2KR
11	7	5.1	1035	1	POL_HV2NR
12	7	5.1	1036	1	POL_HV2RO
13	7	5.1	1049	1	POL_HV2GI
14	7	5.1	1055	1	POL_HV2ST
15	7	5.1	1073	1	POL_HV2D1
16	7	5.1	1142	1	POL_HV2BE
17	7	5.1	3163	1	POLG_TUWVO
18	7	5.1	3164	1	POLG_TUWVO
19	6	4.4	63	1	YPTA_BACSU
20	6	4.4	85	1	YKK2_CAEEL
21	6	4.4	90	1	POLG_GSNV
22	6	4.4	128	1	GCSE_ECOLI
23	6	4.4	137	1	RK19_NEPOL
24	6	4.4	138	1	RBS_GALSV
25	6	4.4	146	1	PABZ_PSEAE
26	6	4.4	153	1	HYCA_ECOLI
27	6	4.4	153	1	YORZ_LISMO
28	6	4.4	158	1	RRT_ODOST
29	6	4.4	160	1	RS7A_AOUAE
30	6	4.4	160	1	RS7B_AOUAE
31	6	4.4	175	1	HER1_CAEEL
32	6	4.4	183	1	VH96_ARCFU
33	6	4.4	193	1	SAP3_HUMAN
71	353	4.4	353	1	HEMA_INBRA
72	353	4.4	353	1	PSBA_MESVI
73	361	4.4	361	1	MTD_MESCR
74	363	4.4	363	1	HEMA_INBSL
75	365	4.4	365	1	HEMA_INBSL
76	366	4.4	366	1	HEMA_INBSL
77	368	4.4	368	1	ILVE_MYCTU
78	377	4.4	377	1	MTC3_CHVNI
79	392	4.4	392	1	BCAM_HUMAN
80	392	4.4	392	1	GCST_CHICK
81	392	4.4	392	1	RPA2_SULAC
82	393	4.4	393	1	ILIS_CERAE
83	396	4.4	396	1	CSA_HUMAN
84	396	4.4	396	1	EFYU_MYCLE
85	397	4.4	397	1	EFYU_PLARO
86	397	4.4	397	1	RL3_DICDI
87	398	4.4	398	1	ILIS_HUMAN
88	407	4.4	407	1	Y173_AOUAE
89	412	4.4	412	1	PT56_YEAST
90	416	4.4	416	1	YMG5_CAEEL
91	425	4.4	425	1	YGGP_ECOLI
92	428	4.4	428	1	PROB_YEAST
93	434	4.4	434	1	TA47_TREPA
94	437	4.4	437	1	PAK_ECOLI
95	452	4.4	452	1	PAK_HUMAN
96	457	4.4	457	1	GA18_KLUFA
97	462	4.4	462	1	CATC_MOUSE
98	469	4.4	469	1	YH89_METUA
99	480	4.4	480	1	HD11_XENLA
100	480	4.4	480	1	HD12_XENLA
101	480	4.4	480	1	HD11_CHICK
102	481	4.4	481	1	6P6D_DROME
103	481	4.4	481	1	6P6D_DROME
104	482	4.4	482	1	ALM2_PANMI
105	487	4.4	487	1	YOM5_CAEEL
106	489	4.4	489	1	PABA_BACSU
12440					influenza a
mesembryant					
P93257					
influenza b					
P12442					
influenza b					
P12441					
influenza b					
010399					mycobacteri
P10835					chlorella v
015882					humo saplen
P28537					gallus gall
P11514					seri
029612					cercopithec
013216					humo saplen
P30768					mycobacteri
P72231					planobispor
P34113					dictyosteli
P27930					humo saplen
067720					aquific aeo
P25270					saccharomyc
020932					caenorhabdi
P25048					escherichia
P32264					saccharomyc
P29723					treponema p
P76085					escherichia
013685					humo saplen
006433					kluyveromyc
P97821					mus musculu
058299					methanococc
091695					xenopus lae
042227					xenopus lae
P56517					gallus gall
P41572					drosophila
P41573					drosophila
P34106					paniscum mli
P30651					caenorhabdi
P37967					bacillus su

107	6	4.4	500	1	ANP1_YEAST	P32629	saccharomyc	180	6	4.4	950	1	CDAD_HUMAN	O9y513	homo sapien
108	6	4.4	526	1	CAP_YEAST	P17555	saccharomyc	181	6	4.4	950	1	CDAD_HUMAN	O9y518	homo sapien
109	6	4.4	529	1	YL27_CAEEL	P34470	caenorhabditi	182	6	4.4	950	1	CDAD_HUMAN	O9un73	homo sapien
110	6	4.4	534	1	CH60_GALISU	P28256	galdieria s	183	6	4.4	950	1	CDAD_HUMAN	O9y515	homo sapien
111	6	4.4	536	1	TMAS_HUMAN	O15131	homo sapien	184	6	4.4	950	1	CDAD_HUMAN	O9y515	homo sapien
112	6	4.4	536	1	INR2_SHEEP	O95207	ovis aries	185	6	4.4	950	1	CDAD_HUMAN	O9y515	homo sapien
113	6	4.4	533	1	YF61_METJA	O58956	methanococc	186	6	4.4	963	1	CDCL_HUMAN	O9h158	homo sapien
114	6	4.4	574	1	HEMA_INBMD	P03461	influenza b	187	6	4.4	966	1	PHS1_SOLTU	P04045	homo sapien
115	6	4.4	575	1	HEMA_INBHK	P10448	influenza b	188	6	4.4	1007	1	CDCL_HUMAN	O9y514	homo sapien
116	6	4.4	575	1	HEMA_INBHK	P03462	influenza b	189	6	4.4	1018	1	HMW1_MYCPN	O50365	mycoplasma
117	6	4.4	576	1	HEMA_INBME	P09766	influenza b	190	6	4.4	1025	1	ADAI_YEAST	P38065	saccharomyc
118	6	4.4	578	1	HEMA_INBVI	P09765	influenza b	191	6	4.4	1120	1	RPOM_SCHPO	O13993	schizosacch
119	6	4.4	583	1	HEMA_INBVI	P10757	influenza b	192	6	4.4	1132	1	TERP_HUMAN	O14746	homo sapien
120	6	4.4	583	1	HEMA_INBVI	P10757	influenza b	193	6	4.4	1211	1	DP3A_HELPJ	O9z4f9	homo sapien
121	6	4.4	583	1	HEMA_INBVI	P10757	influenza b	194	6	4.4	1211	1	DP3A_HELPJ	P56157	helicobacte
122	6	4.4	584	1	HEMA_INBVI	P17504	influenza b	195	6	4.4	1225	1	Y309_MYCG	P47351	mycoplasma
123	6	4.4	585	1	HEMA_INBVI	P17504	influenza b	196	6	4.4	1227	1	LAER_HUMAN	P51826	homo sapien
124	6	4.4	585	1	HEMA_INBVI	P22092	influenza b	197	6	4.4	1486	1	MURK_ECOLI	P22523	escherichia
125	6	4.4	585	1	HEMA_INBVI	P22092	influenza b	198	6	4.4	1762	1	DPQO_HUMAN	O75417	homo sapien
126	6	4.4	585	1	HEMA_INBVI	P22092	influenza b	199	6	4.4	1871	1	PLX4_HUMAN	P51805	homo sapien
127	6	4.4	627	1	YHAB_YEAST	P38750	saccharomyc	200	6	4.4	1947	1	MYSC_CAEEL	P12845	caenorhabditi
128	6	4.4	627	1	YHAB_YEAST	P38750	saccharomyc	201	6	4.4	3079	1	IRR2_YEAST	P19158	saccharomyc
129	6	4.4	628	1	HNFA_MOUSE	P22361	mus musculus	202	6	4.4	3519	1	OLB6_STRAT	O07017	streptomyces
130	6	4.4	632	1	HNFA_MOUSE	P15257	rattus norv	203	6	4.4	4369	1	RYNC_RABIT	P30957	oryctolagus
131	6	4.4	638	1	KRAF_XENLA	P09360	xenopus lae	204	6	4.4	4969	1	BOVR_BOTJA	P22028	bohrrops ja
132	6	4.4	651	1	HS7D_DROME	P11147	drosofila	205	6	3.7	32	1	PA2_RHONO	P43318	rhophilama n
133	6	4.4	651	1	SYM_METJA	O58659	methanococc	206	6	3.7	33	1	RLZ1_XENLA	P43318	rhophilama n
134	6	4.4	662	1	SYM_METJA	O58659	methanococc	207	6	3.7	33	1	TYBN_HUMAN	O99406	homo sapien
135	6	4.4	664	1	SYM_BACSU	P39217	baecillus su	208	6	3.7	49	1	THP1_BOVIN	P01249	bos taurus
136	6	4.4	664	1	SYM_BACSU	P39217	baecillus su	209	6	3.7	49	1	THP2_BOVIN	P01250	bos taurus
137	6	4.4	668	1	YKCA_CAEEL	P42083	caenorhabditi	210	6	3.7	49	1	THPS_BOVIN	P01251	bos taurus
138	6	4.4	688	1	VIDA_AGRT6	P09817	agrobacteri	211	6	3.7	52	1	RUBR_DESGI	P00270	desulfovibr
139	6	4.4	696	1	Y195_SYNY3	P74101	synchocyst	212	6	3.7	53	1	IBB2_WHEAT	O98864	triticum ae
140	6	4.4	705	1	ADPG_RAT	O62847	rattus norv	213	6	3.7	54	1	RLB3_XYLEFA	O99621	xytelia fas
141	6	4.4	705	1	ADPG_RAT	O62847	rattus norv	214	6	3.7	54	1	STP1_MOUSE	P10856	mus musculus
142	6	4.4	706	1	ADPG_RAT	O62847	rattus norv	215	6	3.7	54	1	STP1_MOUSE	P03317	rattus norv
143	6	4.4	706	1	ADPG_RAT	O62847	rattus norv	216	6	3.7	54	1	Y01K_BP7A	P33228	bacterioph
144	6	4.4	710	1	RNR_THEMA	O9w211	thermotoga	217	6	3.7	59	1	MTPE_SULAC	P23039	sulfolobus
145	6	4.4	715	1	ZP2_CAVEA	O9w211	thermotoga	218	6	3.7	61	1	RLZ1_PIG	P4666	sus scrofa
146	6	4.4	721	1	DNK_APHHA	O52960	aphanochece	219	6	3.7	63	1	PERC_SUNNU	P81498	suncus murti
147	6	4.4	728	1	HGF_MOUSE	O08048	mus musculus	220	6	3.7	68	1	YFPC_ECOLI	P33326	escherichia
148	6	4.4	744	1	GYRA_AQUAE	P17945	rattus norv	221	6	3.7	71	1	HPIS_PARSB	P00264	paracoccus
149	6	4.4	748	1	MURA_MOUSE	P16332	mus musculus	222	6	3.7	76	1	RP0Z_AQUAE	O66570	aquiflex aeo
150	6	4.4	750	1	MURA_MOUSE	P22033	homo sapien	223	6	3.7	79	1	Y607_METJA	O58024	methanococc
151	6	4.4	751	1	MURA_MOUSE	P22033	homo sapien	224	6	3.7	80	1	FER1_METJA	O60368	methanococc
152	6	4.4	761	1	STAT_DROME	P11126	bacterioph	225	6	3.7	82	1	YBIM_HERAV	P25237	herpetosiph
153	6	4.4	769	1	VPI_BPPH6	P30851	shigella fl	226	6	3.7	83	1	YELM_HERAV	P25281	herpetosiph
154	6	4.4	770	1	RNR_SHIFL	P39961	saccharomyc	227	6	3.7	85	1	CAID_BOVIN	O21976	bos taurus
155	6	4.4	794	1	YE14_YEAST	O63418	rattus norv	228	6	3.7	85	1	ACTO_ENTHI	O15602	entamoeba h
156	6	4.4	797	1	CDR3_RAT	O50288	mycoplasma	229	6	3.7	87	1	GBG_IOLFO	O01821	loiligo forb
157	6	4.4	798	1	YC00_MYCPN	P08468	saccharomyc	230	6	3.7	88	1	GLR2_SYNY3	P73492	synchocyst
158	6	4.4	800	1	P111_YEAST	P57126	buchnera ap	231	6	3.7	89	1	DBHB_NEIMA	O91416	neisseria m
159	6	4.4	803	1	GYRB_BUCAL	P21499	escherichia	232	6	3.7	89	1	TATA_HAEIN	P50404	haemophilus
160	6	4.4	813	1	RNR_ECOLI	P33388	salmonella	233	6	3.7	91	1	RS10_METJA	O58326	methanococc
161	6	4.4	814	1	SEFC_SALEN	P36774	myxococcus	234	6	3.7	92	1	PEIC_ECOLI	P14039	methanococc
162	6	4.4	826	1	LOM2_MYXXA	O43374	homo sapien	235	6	3.7	92	1	PCP1_BPP22	P33159	escherichia
163	6	4.4	834	1	RGS5_HUMAN	P48764	homo sapien	236	6	3.7	92	1	VC02_SPVKA	P32230	swinepox vi
164	6	4.4	834	1	RGS5_HUMAN	P48764	homo sapien	237	6	3.7	93	1	HMCI_METPA	P06116	methanocarc
165	6	4.4	862	1	LOX1_HORVU	P29114	hordium vul	238	6	3.7	94	1	RL31_PYRAB	O9y417	pyrococcus
166	6	4.4	875	1	IMB1_RAT	P53296	rattus norv	239	6	3.7	94	1	RL35_PIG	O28361	sus scrota
167	6	4.4	876	1	IMB1_RAT	P53296	rattus norv	240	6	3.7	94	1	YC2M_HERAV	P25278	herpetosiph
168	6	4.4	876	1	IMB1_RAT	P53296	rattus norv	241	6	3.7	94	1	ATP2_YEAST	P19436	thermus aqu
169	6	4.4	876	1	IMB1_RAT	P53296	rattus norv	242	6	3.7	95	1	DBH_THETH	P19436	thermus aqu
170	6	4.4	901	1	IMB1_MOUSE	P70168	mus musculus	243	6	3.7	96	1	CTCI_ACTIM	O33947	actinobact
171	6	4.4	910	1	PHSG_YEAST	P06738	saccharomyc	244	6	3.7	96	1	PER_SYNY1	P00255	synchococc
172	6	4.4	936	1	CDAY_HUMAN	O9y517	homo sapien	245	6	3.7	96	1	XTLB_ARTS7	P26909	actinobacte
173	6	4.4	937	1	CDAY_HUMAN	O9y517	homo sapien	246	6	3.7	96	1	TGGU_ECOLI	P2060	escherichia
174	6	4.4	941	1	CDAC_HUMAN	O9un75	homo sapien	247	6	3.7	97	1	FER_SYNEL	P00256	synchococc
175	6	4.4	948	1	CDAC_HUMAN	O9un75	homo sapien	248	6	3.7	98	1	FER2_RAPSA	P14937	raphanus sa
176	6	4.4	948	1	CDAC_HUMAN	O9y512	homo sapien	249	6	3.7	98	1	KRFI_LARNO	P02451	larus novae
177	6	4.4	949	1	CDAB_HUMAN	O9y511	homo sapien	250	6	3.7	99	1	SECY_BACST	P28650	baecillus st
178	6	4.4	949	1	CDAB_HUMAN	O9y511	homo sapien	251	6	3.7	99	1	POL_SIVAZ	P12500	simian immu
179	6	4.4	949	1	IF2_HELPJ	O9zma46	helicobacte	252	6	3.7	100	1	POL_SIVAZ	P12500	simian immu

253	5	3.7	100	1	POL_STIVA3	P12501	stlmian	immu	326	5	3.7	128	1	RL26_CHICK	P47832	gallus	galli
254	5	3.7	100	1	RL23_BUCAI	P57589	buchnera	ap	327	5	3.7	129	1	GLNR_BACCE	P19083	bacillus	ce
255	5	3.7	101	1	B3AR_PIG	O95252	sus	scrofa	328	5	3.7	129	1	RS6E_ARCFU	O29739	archaeoglob	
256	5	3.7	101	1	SMD3_YEAST	P43321	saccharomyc		329	5	3.7	129	1	VE11_VACCV	P21051	vaccinia	vi
257	5	3.7	101	1	URE2_HAEIN	P43392	haemophilus		330	5	3.7	129	1	VE11_VARY	P33822	variola	vir
258	5	3.7	101	1	YD31_MYCTU	O10642	mycobacteri		331	5	3.7	130	1	TYB8_MOUSE	P06321	mus	musculus
259	5	3.7	102	1	ARSC_NEIGO	P93354	neisseria	g	332	5	3.7	130	1	YB12_MYCPN	P75450	mycoplasma	
260	5	3.7	102	1	CYC3_DESDO	P00134	desulfovibr		333	5	3.7	131	1	PER_ZAPVU	O21135	zaprionus	t
261	5	3.7	102	1	GLRX_RICCO	P55143	ricinus	com	334	5	3.7	131	1	RI7A_SCHPO	O42984	schizosacch	
262	5	3.7	104	1	CYC_ATESP	P00003	ateles	sp..	335	5	3.7	131	1	YOHF_BACSU	P01022	rana	catesb
263	5	3.7	104	1	CYC_HUMAN	P00001	homo	sapien	336	5	3.7	132	1	HBAM_RANCA	O96716	schizosacch	
264	5	3.7	104	1	CYC_MACMU	P00002	macaca	mula	337	5	3.7	132	1	RL7B_SCHPO	O42106	marke	japon
265	5	3.7	104	1	RPOZ_STRPY	P82577	streptococc		338	5	3.7	133	1	CLX1_NARJA	P51260	porphyra	pu
266	5	3.7	105	1	ARSR_BACSU	P45949	bacillus	su	339	5	3.7	134	1	ATPE_PORFU	O18180	homo	sapien
267	5	3.7	105	1	COTW_BACSU	O08310	bacillus	su	340	5	3.7	134	1	CLX1_HUMAN	O64276	mus	musculus
268	5	3.7	105	1	Y613_ARCFU	O29642	archaeoglob		341	5	3.7	134	1	CLX1_MOUSE	O13329	homo	sapien
269	5	3.7	106	1	BOLA_VIBCH	O9KPS0	vibrio	chol	342	5	3.7	134	1	CLX2_HUMAN	O42105	marke	japon
270	5	3.7	106	1	RNFI_GIBRU	P10282	glibberella		343	5	3.7	134	1	CLX2_NARJA	P53716	candida	alb
271	5	3.7	106	1	Y094_HAEIN	P40939	haemophilus		344	5	3.7	134	1	YB5_CANML	P06285	marchantia	
272	5	3.7	106	1	YAVC_RHISN	O53211	rhizobium	s	345	5	3.7	135	1	ATPE_MARPO	O01469	homo	sapien
273	5	3.7	106	1	YBC8_YEAST	P38202	saccharomyc		346	5	3.7	135	1	FABE_HUMAN	O08450	clostridium	
274	5	3.7	107	1	RLA1_LEIPE	O46313	leishmania		347	5	3.7	136	1	DEF_CLOBE	P01759	mus	musculus
275	5	3.7	108	1	Y203_METUA	O60268	methanococc		348	5	3.7	136	1	HV15_MOUSE	P55837	actinobacil	
276	5	3.7	108	1	FEL2_FELCA	P30440	felis	silve	349	5	3.7	136	1	RL16_ACTAC	P02414	eschericchia	
277	5	3.7	109	1	LVIF_HUMAN	P04208	homo	sapien	350	5	3.7	136	1	RL16_ECOLI	P44354	haemophilus	
278	5	3.7	109	1	RS17_METVA	P14042	methanococc		351	5	3.7	136	1	RL16_HAEIN	P75149	mycoplasma	
279	5	3.7	109	1	RH10_EMENT	P29429	emeritella		352	5	3.7	136	1	Y441_MYCPN	O62250	caenorhabdi	
280	5	3.7	109	1	VGLI_HSVSB	P36343	simian	hep	353	5	3.7	136	1	Y452_CAEEL	P01755	mus	musculus
281	5	3.7	109	1	YF39_METUA	O58934	methanococc		354	5	3.7	137	1	HV11_MOUSE	P01822	mus	musculus
282	5	3.7	110	1	EMS2_LYTYA	P28773	lytechinus		355	5	3.7	137	1	HV46_MOUSE	P47320	mycoplasma	
283	5	3.7	110	1	RLA4_YEAST	P02400	saccharomyc		356	5	3.7	137	1	Y074_MYCGE	O51204	botreilia	bu
284	5	3.7	110	1	YCKD_BACSU	P42402	bacillus	su	357	5	3.7	137	1	Y186_BORBU	P74755	synechococc	
285	5	3.7	111	1	HV35_MOUSE	P01804	mus	musculi	358	5	3.7	138	1	PSBU_SYN2P	P01751	mus	musculus
286	5	3.7	111	1	RLA1_CAEEL	P91913	caenorhabdi		359	5	3.7	139	1	HV07_MOUSE	O60334	methanococc	
287	5	3.7	111	1	YC91_MYCTU	O10617	mycobacteri		360	5	3.7	139	1	Y024_METUA	P08985	dirosophila	
288	5	3.7	112	1	ACPM_SCHPO	O10217	schizosacch		361	5	3.7	140	1	H2AV_DROME	P33848	varitola	yir
289	5	3.7	112	1	PEDB_PEDAC	P36496	pediococcus		362	5	3.7	140	1	Y431_VARY	O29019	archaeoglob	
290	5	3.7	112	1	RLA1_DROME	P08570	drosophila		363	5	3.7	140	1	Y649_ARCFU	O15392	homo	sapien
291	5	3.7	113	1	FLIT_BACSU	P39740	bacillus	su	364	5	3.7	142	1	B1R5_HUMAN	O92793	chlamydia	p
292	5	3.7	114	1	PSPP_PAPAN	O28767	papio	anubi	365	5	3.7	142	1	Y742_CHLPI	P46888	eschericchia	
293	5	3.7	115	1	RL19_BACSU	O31742	bacillus	su	366	5	3.7	142	1	YECG_ECOLI	P12193	rattus	norv
294	5	3.7	115	1	RL24_SYNY3	P73309	synechocyst		367	5	3.7	143	1	DHSB_RAT	O9795	drosophila	
295	5	3.7	117	1	PRD1_CAEEL	O17827	caenorhabdi		368	5	3.7	143	1	PRD2_DROME	P14032	methanococc	
296	5	3.7	117	1	PRDB_PYROH	O58268	pyrococcus		369	5	3.7	143	1	RL15_METVA	O95990	homo	sapien
297	5	3.7	117	1	SPT4_HUMAN	O16550	homo	sapien	370	5	3.7	144	1	DRRI_HUMAN	O95990	homo	sapien
298	5	3.7	117	1	YCJD_ECOLI	P45736	eschericchia		371	5	3.7	144	1	NAPV_HELPY	P43313	helicobacte	
299	5	3.7	118	1	HV39_MOUSE	P01809	mus	musculi	372	5	3.7	144	1	NAPV_HELPY	P75090	mycoplasma	
300	5	3.7	118	1	RLA3_ORYSA	P56724	oryza	sativ	373	5	3.7	144	1	RPOE_MYCPN	P24120	oryza	sativ
301	5	3.7	118	1	YG35_BRPLH	O04769	lactococcus		374	5	3.7	144	1	SODM_BRARL	P28761	branchiosto	
302	5	3.7	119	1	WNIA_PLEUL	P28131	plethodon	j	375	5	3.7	144	1	Y100_AOUAE	O67669	aquilex	aeo
303	5	3.7	119	1	YXS9_CAEEL	O10026	caenorhabdi		376	5	3.7	144	1	RL26_HUMAN	P12749	rattus	norv
304	5	3.7	120	1	H203_MOUSE	P01947	mus	musculi	377	5	3.7	145	1	RL26_HUMAN	O33603	streptococc	
305	5	3.7	121	1	H2B1_TETTH	P08993	tetrahymena		378	5	3.7	145	1	SODM_RAT	O54210	streptococc	
306	5	3.7	121	1	H2B2_TETTH	P08994	tetrahymena		379	5	3.7	145	1	SODM_STRAI	O54210	streptococc	
307	5	3.7	121	1	HV01_MOUSE	P01745	mus	musculi	380	5	3.7	145	1	SODM_STROB	O54233	streptococc	
308	5	3.7	122	1	RL35_HUMAN	P42766	homo	sapien	381	5	3.7	145	1	SODM_STRIN	O54286	streptococc	
309	5	3.7	122	1	RL35_RAT	P17078	rattus	norv	382	5	3.7	145	1	SODM_STRO	O33785	streptococc	
310	5	3.7	122	1	SSB_BPB03	O37885	bacterioph	a	383	5	3.7	145	1	SODM_STRSL	O01095	desulfovibr	
311	5	3.7	122	1	YEEU_ECOLI	P76364	eschericchia		384	5	3.7	146	1	FLAV_DESGI	P47657	mycoplasma	
312	5	3.7	123	1	YB8F_YEAST	P38357	saccharomyc		385	5	3.7	146	1	RL13_MYCGE	O39411	brassica	ra
313	5	3.7	123	1	YXK6_YEAST	P53077	saccharomyc		386	5	3.7	146	1	YBPF_BRARL	P50732	bacillus	su
314	5	3.7	123	1	YUS4_YEAST	P46984	saccharomyc		387	5	3.7	147	1	YBPF_BACSU	P45594	dirosophila	
315	5	3.7	123	1	YROP_HALHA	O24785	halobacteri		388	5	3.7	148	1	CADF_DROME	O94083	mus	musculi
316	5	3.7	124	1	CHEY_PSEAE	O51455	pseudomonas		389	5	3.7	148	1	D112_MOUSE	O64037	bacterioph	a
317	5	3.7	124	1	MUTT_BUCAI	P57298	buchnera	ap	390	5	3.7	148	1	DSBH_BPSPC	O92949	faqus	sylla
318	5	3.7	124	1	PER_HTRPI	O25109	hittodrosop		391	5	3.7	149	1	LSM4_FAGSY	P40620	vicia	faba
319	5	3.7	124	1	VA31_YACCC	P21096	vaccinia	vi	392	5	3.7	149	1	HMGL_VICFA	P18149	francisella	
320	5	3.7	124	1	VA31_VACCV	P24760	vaccinia	vi	393	5	3.7	149	1	ML17_FFRATU	O67561	aquilex	aeo
321	5	3.7	124	1	YEF7_SCHPO	O14068	schizosacch		394	5	3.7	149	1	RL15_AOUAE	O58329	methanococc	
322	5	3.7	124	1	YHCC_BACSU	P54587	bacillus	su	395	5	3.7	149	1	Y919_METUA	O96730	lactococcus	
323	5	3.7	125	1	CGB0_HUMAN	O9Y3B4	homo	sapien	396	5	3.7	150	1	DUT_LACIA	P11801	homo	sapien
324	5	3.7	126	1	RS6E_METTH	O26560	methanobact		397	5	3.7	150	1	KPSH_HUMAN	P13902	saccharomyc	
325	5	3.7	127	1	SYUR_HUMAN	O9N250	homo	sapien	398	5	3.7	151	1	INO4_YEAST			

399	5	3.7	151	1	RL13_SYNY3	P73294 synechocyst	472	5	3.7	175	1	YF49_MYCTU	Q10777 mycobacteri
400	5	3.7	152	1	MSCL_CLOPE	P53380 clostridium	473	5	3.7	176	1	TRAF_AGR6	Q44364 agrobacteri
401	5	3.7	152	1	Y554_METUA	Q57974 methanococc	474	5	3.7	177	1	BTC_MOUSE	Q05928 mus musculu
402	5	3.7	152	1	YB83_METUA	Q58878 methanococc	475	5	3.7	177	1	RL6_METTH	Q26127 methobact
403	5	3.7	153	1	Y264_METUA	Q57712 methanococc	476	5	3.7	177	1	YAI6_SCHPO	Q09688 schizosacch
404	5	3.7	153	1	YEH3_PSEAE	Q9hub0 pseudomonas	477	5	3.7	177	1	YNIW_AZOOH	P22177 azotobacter
405	5	3.7	154	1	BFRA_NEIMA	P56998 neisseria m	478	5	3.7	178	1	BTC_HUMAN	P35070 homo sapien
406	5	3.7	154	1	BFRA_NEIMA	P72080 neisseria m	479	5	3.7	178	1	RBS_TRIRP	P17673 trifolium r
407	5	3.7	154	1	RR7_SPTOL	P82129 splinacia ol	480	5	3.7	178	1	SIGV_BACSU	P94370 bacillus su
408	5	3.7	154	1	YK01_AERPE	Q9vnd8 aeropyrum p	481	5	3.7	178	1	VG20_BPLH	Q04763 lactococcus
409	5	3.7	154	1	YH13_MARPO	P38457 marchantia	482	5	3.7	179	1	NUSG_STRPY	P82547 streptococc
410	5	3.7	154	1	YWEA_BACSU	P36632 bacillus su	483	5	3.7	179	1	Y502_STRO	Q9x928 streptococc
411	5	3.7	155	1	RL21_PYUST	P49667 pyura stolo	484	5	3.7	179	1	YAI1_ECOLI	P46122 escherichia
412	5	3.7	155	1	RR7_ARATH	P56800 arabidopsis	485	5	3.7	180	1	HMGI_CRIGR	P07156 cricetus
413	5	3.7	155	1	RR7_CUSEU	P46292 cusculta eur	486	5	3.7	180	1	RBS2_PEA	P00869 plium sativ
414	5	3.7	155	1	RR7_CUSRE	P34832 cusculta ref	487	5	3.7	180	1	RBS3_PEA	P07689 plium sativ
415	5	3.7	155	1	RR7_EPIVI	P30057 epifagus vi	488	5	3.7	180	1	RBS_MEDSA	Q65194 medicago sa
416	5	3.7	155	1	RR7_EUGGR	P02360 euglena gra	489	5	3.7	180	1	RL15_LEPIN	Q9ydl7 leptospira
417	5	3.7	155	1	RR7_MARPO	P06360 marchantia	490	5	3.7	180	1	VG20_BPMVA	Q04764 lactococcus
418	5	3.7	155	1	RR7_PINTH	P41652 pinus thunb	491	5	3.7	180	1	Y16A_MYCMT	Q50239 mycoplasma
419	5	3.7	155	1	RR7_SOYBN	P07135 glycine max	492	5	3.7	180	1	YH21_MARPO	P38464 marchantia
420	5	3.7	155	1	RR7_TOBAC	P06361 nicotiana t	493	5	3.7	181	1	ATP3_HUMAN	P18847 homo sapien
421	5	3.7	155	1	RS15_HAIMA	P05762 haloarcula	494	5	3.7	181	1	ATP3_MOUSE	Q06765 mus musculu
422	5	3.7	156	1	SSRP_BACSU	Q32230 bacillus su	495	5	3.7	181	1	ATP3_RAT	P29596 rattus norv
423	5	3.7	157	1	Y117_YEAST	P40502 saccharomyc	496	5	3.7	181	1	RBS1_NITCSY	P22433 nicotiana s
424	5	3.7	158	1	FMAA_BACNO	P02375 bacteroides	497	5	3.7	181	1	RL5_METVA	P14029 methanococc
425	5	3.7	158	1	ILVH_LACLA	Q02140 lactococcus	498	5	3.7	181	1	RM06_ACACA	P46765 acanthamoeb
426	5	3.7	159	1	RL21_HUMAN	P46178 homo sapien	499	5	3.7	182	1	HSLV_RICPR	Q9xdk9 rickettsia
427	5	3.7	159	1	RL21_MOUSE	Q09167 mus musculu	500	5	3.7	182	1	YLP3_CAEL	P34383 caenorhabdi
428	5	3.7	159	1	RL21_RAT	P20280 rattus norv	501	5	3.7	182	1	YOPO_YEREN	P27474 versinia en
429	5	3.7	159	1	Y268_BORBU	Q44756 borrelia bu	502	5	3.7	183	1	APR_ECOLI	P07672 escherichia
430	5	3.7	160	1	FMA1_BACNO	P17823 bacteroides	503	5	3.7	184	1	ETS3_DROME	P29774 drosophila
431	5	3.7	160	1	FMA2_BACNO	P17824 bacteroides	504	5	3.7	185	1	CBX1_HUMAN	P23197 homo sapien
432	5	3.7	160	1	FMA3_BACNO	P27691 bacteroides	505	5	3.7	185	1	PF03_CAEL	Q10804 caenorhabdi
433	5	3.7	160	1	FMA4_BACNO	P17822 bacteroides	506	5	3.7	185	1	YALI_TRYBB	P17960 trypanosoma
434	5	3.7	160	1	YCX3_ASTIO	P34777 astasia lon	507	5	3.7	186	1	CHS2_USTMA	P30599 ustilago ma
435	5	3.7	160	1	YDCD_ECOLI	P31991 escherichia	508	5	3.7	186	1	WOS2_SCHPO	Q11118 schizosacch
436	5	3.7	160	1	YEMO_YEAST	P40019 saccharomyc	509	5	3.7	187	1	ALL1_HORSE	Q95118 equus cabal
437	5	3.7	161	1	FMA3_BACNO	P27689 bacteroides	510	5	3.7	187	1	DEF_SYNY3	P73441 synechocyst
438	5	3.7	161	1	FMA4_BACNO	P27906 bacteroides	511	5	3.7	187	1	PTPA_PSEAE	Q58641 pseudomonas
439	5	3.7	162	1	VENV_EAV	P28991 equine arte	512	5	3.7	188	1	DCPD_BPT2	P00814 chlamydia m
440	5	3.7	162	1	Y480_TREPA	Q83493 treponema p	513	5	3.7	188	1	VP21_TBSV8	P50629 tomato bush
441	5	3.7	164	1	PHAL_SYNPP	Q02179 synechococc	514	5	3.7	188	1	YEBB_SCHPO	Q14076 schizosacch
442	5	3.7	164	1	PHAL_SYNPP	Q02179 synechococc	515	5	3.7	189	1	CHS2_XYIIB	P30604 xylophya b
443	5	3.7	164	1	PHAL_SYNPP	Q02179 synechococc	516	5	3.7	189	1	VP21_AMCV	P15961 artichoke m
444	5	3.7	164	1	PHAL_SYNPP	Q02179 synechococc	517	5	3.7	189	1	VP21_TBSVA	P50630 tomato bush
445	5	3.7	164	1	PHAL_SYNPP	Q02179 synechococc	518	5	3.7	189	1	VP21_TBSVB	P50631 tomato bush
446	5	3.7	165	1	YSEB_STACA	P47995 staphylococ	519	5	3.7	190	1	ARE_GIALA	P526991 giardia lam
447	5	3.7	166	1	UTXA_CLODI	P34553 clostridium	520	5	3.7	191	1	RS7_METUA	P54063 methanococc
448	5	3.7	167	1	FLIT_CAUCR	P34008 caulobacter	521	5	3.7	192	1	ERP_AQUAE	Q67376 aquifex aeo
449	5	3.7	168	1	BIP3_TOBAC	Q03683 nicotiana t	522	5	3.7	192	1	KADA_METTIC	P43408 methanococc
450	5	3.7	168	1	FMS3_ECOLI	P13488 escherichia	523	5	3.7	192	1	MOBA_PPRHO	Q58708 pyrococcus
451	5	3.7	169	1	Y358_BUCAI	P57439 buchnera ap	524	5	3.7	192	1	PAAD_CHLMO	Q9phx2 chlamydia m
452	5	3.7	169	1	F631_METUA	Q58048 methanococc	525	5	3.7	193	1	DCPD_BPT4	P16006 bacterioph
453	5	3.7	170	1	FMEF_ECOLI	P25394 escherichia	526	5	3.7	193	1	GVE2_HALN1	Q48311 halobacteri
454	5	3.7	170	1	VEAR_HGMVA	P06694 human cytom	527	5	3.7	194	1	RS7_METVA	P14037 methanococc
455	5	3.7	171	1	CD3D_HUMAN	P04334 homo sapien	528	5	3.7	194	1	YH01_ARCEU	Q29261 archaeoglob
456	5	3.7	171	1	RT23_MOUSE	Q9d125 mus musculu	529	5	3.7	194	1	YADN_ECOLI	P37050 escherichia
457	5	3.7	171	1	Y328_AQUAE	Q66665 aquifex aeo	530	5	3.7	195	1	ALIA_YEAST	P32459 saccharomyc
458	5	3.7	171	1	YE11_HAEIN	Q57374 haemophilus	531	5	3.7	195	1	GYRA_FIBSU	P35810 fibroblacter
459	5	3.7	172	1	PHCB_CYACA	Q19909 cyanidium c	532	5	3.7	196	1	CAGS_HELPY	P97227 helicobacte
460	5	3.7	172	1	TCTP_MOUSE	P14701 mus musculu	533	5	3.7	196	1	HP20_TAMAS	Q06575 tamias asia
461	5	3.7	172	1	YB03_MYCPN	P75366 mycoplasma	534	5	3.7	196	1	RK3_ODOST	P49569 odontella s
462	5	3.7	173	1	ERG_LYTYA	Q01414 lytechinus	535	5	3.7	196	1	YPB3_LACLA	P24097 lactococcus
463	5	3.7	173	1	HA34_BRELC	Q99074 bremlia lact	536	5	3.7	197	1	ENGB_ARCEU	Q28943 archaeoglob
464	5	3.7	173	1	LIT2_MOUSE	Q08731 mus musculu	537	5	3.7	197	1	Y060_BPT4	P70827 borrelia bu
465	5	3.7	173	1	YRVS_CAEL	Q09355 caenorhabdi	538	5	3.7	197	1	YF79_ARCEU	P33924 bacterioph
466	5	3.7	174	1	FANG_ECOLI	P20861 escherichia	539	5	3.7	197	1	RAC3_ARATH	Q28693 archaeoglob
467	5	3.7	174	1	GRPE_METTH	Q27350 methanobact	540	5	3.7	198	1	RAC3_ARATH	Q38912 arabidopsis
468	5	3.7	175	1	COAG_CARRO	P03997 carcinoscor	541	5	3.7	199	1	RS8_YEAST	P05754 saccharomyc
469	5	3.7	175	1	IMMB_ECOLI	P12535 mouse adeno	542	5	3.7	199	1	SODF_BABBO	Q15905 babesia bov
470	5	3.7	175	1	IMMB_ECOLI	P22426 escherichia	543	5	3.7	199	1	YGAT_YEAST	P50083 saccharomyc
471	5	3.7	175	1	RL20_SCHPO	P05732 schizosacch	544	5	3.7	199	1	YGCH_ECOLI	Q46897 escherichia

545	5	3.7	200	1	PCP_PYPAB	Q9uyg9	pyrococcus	618	5	3.7	224	1	GER2_WHEAT	P15290	tritium ae
546	5	3.7	200	1	RECR_CHLMU	Q9pxk4	chlamydia m	619	5	3.7	224	1	KST5_ECOLI	P24586	escherichia
547	5	3.7	200	1	RECR_CHLMU	O84223	chlamydia t	620	5	3.7	224	1	MALA_STRPN	O08510	streptococ
548	5	3.7	200	1	RECR_HAEIN	P44722	haemophilus	621	5	3.7	224	1	RS3_CHLMU	O9pjn0	chlamydia t
549	5	3.7	200	1	RECR_PASMU	P57826	pasteurella	622	5	3.7	224	1	RS3_CHLMU	O84527	chlamydia t
550	5	3.7	200	1	SODM_STRPY	P77957	streptococ	623	5	3.7	224	1	Y119_MENTU	O57583	methanococ
551	5	3.7	200	1	SYST_LYCES	P27058	lycopersico	624	5	3.7	224	1	YF81_MCTU	O50640	mycobacteri
552	5	3.7	201	1	ABP1_MAIZE	P13659	zea mays (m	625	5	3.7	225	1	GP30_BPSP1	O38423	bacterioph
553	5	3.7	202	1	CR2_HORVU	P23252	hordeum vul	626	5	3.7	225	1	KAD2_YEAST	P23546	saccharomyc
554	5	3.7	202	1	SODM_STRMU	P09738	streptococ	627	5	3.7	225	1	RS3_LEPIN	O9xdx0	leptospira
555	5	3.7	202	1	VANX_ENTFA	O47749	enterococcu	628	5	3.7	225	1	Y851_PYRAB	O98220	methanococ
556	5	3.7	203	1	CLPP_MARPO	P12208	marichantia	629	5	3.7	225	1	Y851_PYRAB	O9uyv0	pyrococcus
557	5	3.7	203	1	THGA_ECOLI	P07464	escherichia	630	5	3.7	227	1	TPIS_PYRMO	P55533	pyrococcus
558	5	3.7	203	1	YBM4_YEAST	P38068	saccharomyc	631	5	3.7	227	1	UBU_DRONE	P35122	dirosophila
559	5	3.7	203	1	YKVA_YEAST	P36036	saccharomyc	632	5	3.7	227	1	YKVA_METTF	P29577	methanobact
560	5	3.7	204	1	UBCX_PICPA	P49486	saccharomyc	633	5	3.7	228	1	GLXC_RHIME	O67391	rhizobium m
561	5	3.7	205	1	GAR1_YEAST	P28007	saccharomyc	634	5	3.7	228	1	LOLD_BUCAI	P57363	buchnera ap
562	5	3.7	206	1	KAD_AQUAE	O66490	aquifex aeo	635	5	3.7	228	1	TPIS_PYPAB	O9uxx2	pyrococcus
563	5	3.7	206	1	Y817_METUA	O58227	methanococ	636	5	3.7	228	1	Y855_METUA	O58265	methanococ
564	5	3.7	207	1	FLA2_PYRHO	O58283	pyrococcus	637	5	3.7	228	1	Y503_ACIAM	P29087	acidianus a
565	5	3.7	207	1	PSAD_CUCSA	P32869	cucumis sat	638	5	3.7	228	1	YTUB_ERWHE	O47826	erwinia her
566	5	3.7	207	1	SODM_YEREN	P53655	yersinia en	639	5	3.7	229	1	MTN_HAEIN	P51113	haemophilus
567	5	3.7	208	1	ACPD_BACSU	O35022	bacillus su	640	5	3.7	229	1	PEPE_SALTY	P36936	salmonella
568	5	3.7	208	1	HRPW_PSESY	O60236	pseudomonas	641	5	3.7	230	1	Y643_PYRHO	O58377	pyrococcus
569	5	3.7	208	1	MLEY_HUMAN	P14649	homo sapien	642	5	3.7	231	1	TPIS_PYRHO	O59536	pyrococcus
570	5	3.7	210	1	HIS7_MYCLE	Q9x709	mycobacteri	643	5	3.7	231	1	UL71_HSV62	P22346	human herpe
571	5	3.7	210	1	SSH5_YEAST	Q03446	saccharomyc	644	5	3.7	232	1	CASB_PIG	P39037	sus scrofa
572	5	3.7	210	1	XYNA_BACST	P45705	bacillus st	645	5	3.7	232	1	YOD2_CABEL	P00755	sus scrofa
573	5	3.7	210	1	Y041_BP14	P47074	bacterioph	646	5	3.7	232	1	THIQ_ECOLI	P31548	escherichia
574	5	3.7	210	1	YEO9_YEAST	P40052	saccharomyc	647	5	3.7	232	1	VHED_BP13	P20313	bacterioph
575	5	3.7	212	1	KAD_STRPY	P82549	streptococ	648	5	3.7	232	1	VHED_BP13	P30366	bacterioph
576	5	3.7	212	1	UL03_HSV6B	P28942	equine herp	649	5	3.7	232	1	YC68_MYCTU	Q11051	mycobacteri
577	5	3.7	213	1	CAT2_ECOLI	P22615	escherichia	650	5	3.7	233	1	CLC1_YEAST	P17891	saccharomyc
578	5	3.7	213	1	UL71_HSV6U	P22643	human herpe	651	5	3.7	233	1	YOD2_CABEL	P34594	caenorhabdi
579	5	3.7	213	1	XYNA_BACCI	P09850	human herpe	652	5	3.7	236	1	YCBF_ECOLI	P40876	caenorhabdi
580	5	3.7	213	1	XYNA_BACSU	P18429	bacillus su	653	5	3.7	236	1	YIEK_ECOLI	P31470	escherichia
581	5	3.7	214	1	CYB_AGRKO	P92845	agkistrodon	654	5	3.7	237	1	RECA_NEIEG	P14702	neisseria e
582	5	3.7	214	1	CYB_AGRKA	P92852	agkistrodon	655	5	3.7	237	1	RECA_NEIEP	O86403	neisseria p
583	5	3.7	214	1	CYB_BOTAT	P92852	agkistrodon	656	5	3.7	237	1	RECA_NEIEP	O86411	neisseria s
584	5	3.7	214	1	CYB_BOTAT	P92847	bothriopsis	657	5	3.7	237	1	RECA_NEISU	O86411	neisseria s
585	5	3.7	214	1	CYB_BOTSC	P92849	bothriopsis	658	5	3.7	237	1	RECA_NEISU	P26864	marichantia
586	5	3.7	214	1	CYB_CROAT	P92850	crocalus at	659	5	3.7	238	1	GUB_PAEPD	P45797	penicilliu
587	5	3.7	214	1	CYB_CROAT	P92850	crocalus at	660	5	3.7	238	1	PELX_ERMCA	P16530	erwinia car
588	5	3.7	214	1	HMGI_BOVIN	P92857	trimeresuru	661	5	3.7	238	1	RIBB_ARCFU	O28187	archaeoglob
589	5	3.7	214	1	HMGI_BOVIN	P10103	bos taurus	662	5	3.7	238	1	RPE_YEAST	P46965	saccharomyc
590	5	3.7	214	1	HMGI_MOUSE	P09429	homo sapien	663	5	3.7	238	1	YBM9_SCHPO	Q10333	schizosacch
591	5	3.7	214	1	HMGI_MOUSE	P07155	mus musculu	664	5	3.7	239	1	DHSB_PORPU	P80477	porphyra pu
592	5	3.7	214	1	HMGI_MOUSE	P12682	sus scrofa	665	5	3.7	239	1	DHSB_PORPU	P04080	recclinomona
593	5	3.7	214	1	HMGI_MOUSE	O99550	homo sapien	666	5	3.7	239	1	MPUL_ARATH	O91413	arabidopsis
594	5	3.7	215	1	YKL7_YEAST	P28707	autographa	667	5	3.7	239	1	RL32_HALNI	O9hpbt	halobacteri
595	5	3.7	216	1	AKA2_ARATH	P28185	arabidopsis	668	5	3.7	239	1	RP35_BACTK	P26763	halobacteri
596	5	3.7	216	1	YSP4_CABEL	Q10912	caenorhabdi	669	5	3.7	239	1	RPSE_BACSU	P06222	halobacteri
597	5	3.7	217	1	GTN1_SOLTU	P32111	solanum tub	670	5	3.7	239	1	TONB_ECOLI	P02929	escherichia
598	5	3.7	218	1	DNEI_CHLHU	O32001	chlamydomon	671	5	3.7	240	1	OM31_BRUME	O45322	bruceella me
599	5	3.7	218	1	Y052_BORBU	Q51084	borrelia bu	672	5	3.7	240	1	YFIC_HAEIN	P44702	haemophilus
600	5	3.7	218	1	YF81_MYCLE	Q49649	mycobacteri	673	5	3.7	241	1	RECO_SALTY	O56058	salmonella
601	5	3.7	219	1	Y06K_BP14	P13338	bacterioph	674	5	3.7	242	1	CRTW_ALICSP	Q44261	alcaligenes
602	5	3.7	219	1	Y01Y_BACSU	P54536	bacillus su	675	5	3.7	242	1	RECO_ECOLI	P15027	escherichia
603	5	3.7	220	1	HEP1_BACST	P55754	bacillus st	676	5	3.7	242	1	TONB_SALTY	P25945	salmonella
604	5	3.7	220	1	VANR_ENTFA	O47744	enterococcu	677	5	3.7	242	1	TRP2_CVACA	P47493	cyanidium c
605	5	3.7	221	1	GTAL_BOVIN	O28035	bos taurus	678	5	3.7	243	1	TM17_ARATH	O59351	halobacteri
606	5	3.7	221	1	GTAL_PIG	O28035	bos taurus	679	5	3.7	243	1	Y542_CHAPN	O59351	halobacteri
607	5	3.7	221	1	PLL2_MESAU	P51781	sus scrofa	680	5	3.7	245	1	MCT4_RAT	Q52810	chlamydia p
608	5	3.7	221	1	PLL2_RAT	P14059	mesocricetu	681	5	3.7	246	1	Y586_BUCAI	P97592	rattus norv
609	5	3.7	221	1	SEGA_BP14	P09321	rattus norv	682	5	3.7	246	1	YD53_SCHPO	P57696	buchnera ap
610	5	3.7	221	1	Y532_AQUAE	O66814	aquifex aeo	683	5	3.7	247	1	PCNA_HALNI	O41419	schizosacch
611	5	3.7	221	1	YFHB_YEAST	P43502	saccharomyc	684	5	3.7	248	1	PCNA_HALNI	O9hna5	halobacteri
612	5	3.7	222	1	PARA_AGRTU	P07175	agrobacteri	685	5	3.7	248	1	TRPA_PYPAB	P26975	providencia
613	5	3.7	223	1	GTN1_TOBAC	Q03662	nicotiana t	686	5	3.7	249	1	BA72_EUBSP	O9vi99	pyrococcus
614	5	3.7	223	1	GTN2_TOBAC	Q03662	nicotiana t	687	5	3.7	249	1	PCNA_PYPAB	P19337	eubacterium
615	5	3.7	223	1	GTN3_TOBAC	Q03664	nicotiana t	688	5	3.7	249	1	PCNA_PYRHO	O73947	pyrococcus
616	5	3.7	223	1	RS3_CHLBN	O92753	chlamydia p	689	5	3.7	249	1	PCNA_PYRHO	O58398	pyrococcus
617	5	3.7	223	1	SAMP_CANPO	P49255	cavia porce	690	5	3.7	249	1	PCNA_THERM	Q9uwx9	thermococcu

691	5	3.7	249	1	PHOC_MORMO	P28581	morganelia	764	5	3.7	271	1	BLAC_PROVU	P80298	proteus vul
692	5	3.7	250	1	DHSB_CHOIR	P48932	chondirus cr	765	5	3.7	272	1	ERG_MOUSE	P81270	mus musculus
693	5	3.7	250	1	FCEA_MOUSE	P20489	mus musculus	766	5	3.7	272	1	PHEA_METJA	O58054	methanococc
694	5	3.7	250	1	YK67_CAEEL	P34345	caenorhabdit	767	5	3.7	272	1	YK6A_BACSU	O00777	bacillus su
695	5	3.7	251	1	CB24_ARATH	P27521	arabidopsis	768	5	3.7	272	1	YKNS_CAEEL	P32745	caenorhabdit
696	5	3.7	251	1	CRB1_HUMAN	P53674	homo sapien	769	5	3.7	273	1	FOLD_MYCEG	P47259	mycoplasma
697	5	3.7	251	1	IOUR_BACSU	P46337	bacillus su	770	5	3.7	273	1	SC65_YEAST	P23478	saccharomyc
698	5	3.7	252	1	1433_DICDI	P54632	dicyostell	771	5	3.7	274	1	DAPD_BUCAT	P57323	buchnera ap
699	5	3.7	252	1	PSM1_HALVO	O92V66	halobacteri	772	5	3.7	274	1	MEPA_ECOTI	P14007	escherichia
700	5	3.7	252	1	PSM1_HALVO	O58418	methanococc	773	5	3.7	274	1	RECA_NEIFL	O50597	neisseria f
701	5	3.7	252	1	Y830_METJA	O58440	methanococc	774	5	3.7	274	1	RECA_NEIFL	O50597	neisseria f
702	5	3.7	252	1	Y830_METJA	O58440	methanococc	775	5	3.7	274	1	RECA_NEIFL	O50597	neisseria f
703	5	3.7	253	1	Y0XM_BACSU	P40949	bacillus su	776	5	3.7	274	1	YEDQ_ECOTI	O58619	neisseria m
704	5	3.7	253	1	Y0XM_BACSU	P40949	bacillus su	777	5	3.7	275	1	YEDQ_ECOTI	O58619	neisseria m
705	5	3.7	254	1	ADH_DHOWI	O05111	caenorhabdit	778	5	3.7	275	1	KD5A_RICPR	P33399	saccharomyc
706	5	3.7	254	1	YVON_BACSU	O06977	bacillus su	779	5	3.7	275	1	PORE_SOLTH	P40565	solanum tub
707	5	3.7	255	1	143P_ARATH	P42644	arabidopsis	780	5	3.7	275	1	VGIM_PUIMB	P41264	pumila vir
708	5	3.7	255	1	ATP6_TRIRU	O36835	trichophyto	781	5	3.7	276	1	Y578_METJA	O57998	methanococc
709	5	3.7	255	1	HCD2_DROME	O18404	drosophila	782	5	3.7	277	1	KNOB_PLAFD	P03229	plasmidum
710	5	3.7	255	1	THRB_MOUSE	O04999	mus musculus	783	5	3.7	277	1	RS2_CHLPP	O927K9	porphyra pu
711	5	3.7	255	1	LACR_LACLA	P18816	lactococcus	784	5	3.7	277	1	THRG_PORPU	P51361	rattus norv
712	5	3.7	255	1	MYPS_BOVIN	P17667	bos taurus	785	5	3.7	278	1	FASL_RAT	P03627	bacterioph
713	5	3.7	255	1	RECO_BACSU	P42095	bacillus su	786	5	3.7	278	1	VGIL_HCMV1	O66667	human cytom
714	5	3.7	255	1	Y439_PYRHO	O58186	pyrococcus	787	5	3.7	278	1	VGIL_HCMV1	O66667	human cytom
715	5	3.7	256	1	NORE_CHLPP	O928B3	chlamydia p	788	5	3.7	278	1	VGIL_HCMV2	O66667	human cytom
716	5	3.7	256	1	TPYS_VIBMA	P50921	vibrio mali	789	5	3.7	278	1	VGIL_HCMV3	O66667	human cytom
717	5	3.7	256	1	YGBI_HAEIN	P44978	haemophilus	790	5	3.7	278	1	VGIL_HCMV4	O66670	human cytom
718	5	3.7	257	1	Y418_METJA	O57861	methanococc	791	5	3.7	278	1	VGIL_HCMV5	O66671	human cytom
719	5	3.7	258	1	ADH_BACOL	O9a87	bactrocera	792	5	3.7	278	1	VGIL_HCMV6	O66672	human cytom
720	5	3.7	258	1	HIS6_BUCAT	P80869	bacillus su	793	5	3.7	278	1	VGIL_HCMV7	O66673	human cytom
721	5	3.7	258	1	HIS6_BUCAT	P57206	buchnera ap	794	5	3.7	278	1	VGIL_HCMV8	O66674	human cytom
722	5	3.7	258	1	NADC_ARCPR	O28439	archaeoglob	795	5	3.7	278	1	VGIL_HCMV9	O66674	human cytom
723	5	3.7	258	1	RM24_YEAST	P36525	saccharomyc	796	5	3.7	279	1	FASL_MOUSE	P41047	mus musculus
724	5	3.7	258	1	YULB_BACSU	O05261	bacillus su	797	5	3.7	279	1	GR78_PLAFA	P12794	plasmidum
725	5	3.7	259	1	NAHB_PSEPU	O52459	pseudomonas	798	5	3.7	280	1	DHSB_HUMAN	P21912	homo sapien
726	5	3.7	260	1	DH10_ARATH	P42759	arabidopsis	799	5	3.7	281	1	AAC9_MICCH	P28910	micromosp
727	5	3.7	260	1	GRAA_MOUSE	P11032	mus musculus	800	5	3.7	281	1	FASL_HUMAN	P48023	homo sapien
728	5	3.7	260	1	POXJ_XYLFA	O9ph84	xytella fas	801	5	3.7	281	1	NAE1_THEMA	O926B3	thermoptoga
729	5	3.7	260	1	YOGK_BACSU	P46342	bacillus su	802	5	3.7	281	1	PH4H_CHYRO	P30967	chromobacte
730	5	3.7	261	1	143D_SOYBN	O96453	glycine max	803	5	3.7	281	1	THTR_SACPR	P16385	saccharopoi
731	5	3.7	261	1	H156_SYNY3	P74106	synecocyst	804	5	3.7	281	1	XYLF_PSEPU	P23106	pseudomonas
732	5	3.7	261	1	KLK8_RAT	P36374	rattus norv	805	5	3.7	282	1	NADA_APLICA	P28242	aplysia cal
733	5	3.7	261	1	OMPY_CHLMU	O9PK23	chlamydia m	806	5	3.7	282	1	ROC_XENLA	P19600	xenopus lae
734	5	3.7	261	1	OMPY_CHLMU	O84376	chlamydia t	807	5	3.7	282	1	Y32K_BNYVG	P19231	beet necrot
735	5	3.7	261	1	TNPF5_HUMAN	P28965	homo sapien	808	5	3.7	283	1	ARBG_ERWCH	P26211	methanopyru
736	5	3.7	261	1	Y046_METJA	O60354	methanococc	809	5	3.7	283	1	MTD_METKA	P33521	matve strip
737	5	3.7	262	1	APAI_BRARE	O42363	brachydantio	810	5	3.7	283	1	VNS4_MSTV	O50793	mycobacteri
738	5	3.7	262	1	GRAA_HUMAN	P12544	homo sapien	811	5	3.7	284	1	DAPF_BUCAT	P28844	pseudomonas
739	5	3.7	262	1	ISPA_AOUAE	O66952	aquifex aeo	812	5	3.7	284	1	ERR_MYCTU	P28844	pseudomonas
740	5	3.7	262	1	LPXA_HAEIN	P43887	haemophilus	813	5	3.7	284	1	LEP_PSEPU	P28844	pseudomonas
741	5	3.7	262	1	LPXA_PASWU	O9cjk8	pasteurella	814	5	3.7	284	1	RP32_BUCAT	O05385	buchnera ap
742	5	3.7	262	1	MODE_ECOTI	P46930	escherichia	815	5	3.7	284	1	TPM1_SCHNA	O42637	schistosoma
743	5	3.7	262	1	PLCI_CAEEL	O93841	caenorhabdit	816	5	3.7	284	1	DVRB_ZYMONO	O66998	zymomonas m
744	5	3.7	262	1	RNC_MYCEG	P47607	mycoplasma	817	5	3.7	285	1	ALKE_BABBO	O40690	treponema h
745	5	3.7	262	1	S3AD_KLEPN	P08881	klebsiella	818	5	3.7	285	1	FLA3_TREMA	P21992	treponema m
746	5	3.7	263	1	S3AD_ECOTI	P04826	escherichia	819	5	3.7	285	1	FLA3_TREMA	P21992	treponema m
747	5	3.7	264	1	CSH_ARTSP	P32400	arthrobacte	820	5	3.7	285	1	FLB2_TREHY	P21992	treponema p
748	5	3.7	264	1	GIDB_SYNY3	O55787	synecocyst	821	5	3.7	286	1	AGAY_ECOTI	P42908	treponema h
749	5	3.7	264	1	TRPA_SYNY3	P77960	synecocyst	822	5	3.7	286	1	FDHD_WOLSU	P21990	treponema s
750	5	3.7	265	1	PANB_AOUAE	O67783	aquifex aeo	823	5	3.7	286	1	FLA1_TREPA	P21990	treponema s
751	5	3.7	265	1	YEEL_ECOTI	P76346	escherichia	824	5	3.7	286	1	FLA2_TREMA	P21990	treponema m
752	5	3.7	266	1	KLRF_MOUSE	O60653	mus musculus	825	5	3.7	286	1	FLA2_TREMA	P21990	treponema m
753	5	3.7	266	1	YF11_PYRHO	O59180	pyrococcus	826	5	3.7	286	1	FLA2_TREMA	P21990	treponema m
754	5	3.7	266	1	YRHG_BACSU	O05399	bacillus su	827	5	3.7	286	1	YAY8_SCHPO	P44749	homo sapien
755	5	3.7	267	1	KD5A_AOUAE	O64966	aquifex aeo	828	5	3.7	287	1	HUS1_SCHPO	P44749	homo sapien
756	5	3.7	268	1	ETIB_XENLA	P18756	xenopus lae	829	5	3.7	287	1	ESGA_HAEIN	P32856	methanococc
757	5	3.7	268	1	HISJ_NEIGO	O06758	neisseria g	830	5	3.7	288	1	Y134_MYCTU	O50599	mycobacteri
758	5	3.7	268	1	ILIA_CAPII	P79161	capra hircu	831	5	3.7	288	1	Y134_MYCTU	O50599	mycobacteri
759	5	3.7	268	1	KHNL_YEAST	P50112	saccharomyc	832	5	3.7	288	1	Y134_MYCTU	O50599	mycobacteri
760	5	3.7	268	1	THIM_ARCPR	O28204	archaeoglob	833	5	3.7	289	1	HEM3_METHA	O26960	methanobact
761	5	3.7	268	1	Y080_AERPE	O9ya19	aeropyrum p	834	5	3.7	289	1	HEM3_METHA	O26960	methanobact
762	5	3.7	269	1	YHIC_LACLA	O02150	lactococcus	835	5	3.7	289	1	SC13_PICPA	P33024	plachia past
763	5	3.7	270	1	YNF0_YEAST	P53952	saccharomyc	836	5	3.7	289	1	SGCD_MESAU	P97281	mesocricetu

837	5	3.7	289	1	SGCD_MOUSE	P82347	mus musculus	910	5	3.7	308	1	Y040_BP14	P39254	bacterioph
838	5	3.7	289	1	V3IK_TOBSV	P03597	tobacco str	911	5	3.7	308	1	Y222_MYCPN	P75466	mycoplasma
839	5	3.7	289	1	Y097_MYCTO	Q10893	mycobacteri	912	5	3.7	309	1	IFRH_MAIZE	P52560	zea mays (m
840	5	3.7	290	1	ARY1_CHICK	P13913	gallus gall	913	5	3.7	309	1	IKIL_YEAST	P38874	saccharomyc
841	5	3.7	290	1	BIPI_TOBAC	003681	nicotiana t	914	5	3.7	309	1	MAT1_HUMAN	P51948	homo sapien
842	5	3.7	290	1	BLO2_KLEOX	P23954	klebsiella	915	5	3.7	309	1	MAT1_MOUSE	P51949	mus musculus
843	5	3.7	290	1	CHIT_SACER	P14529	saccharopol	916	5	3.7	309	1	MAT1_XENLA	P51951	xenopus lae
844	5	3.7	290	1	EPMO_RAT	P50279	rattus norv	917	5	3.7	309	1	SCA1_TRIVA	P53399	trichomonas
845	5	3.7	290	1	HIS1_SULSO	Q33771	sulfolobus	918	5	3.7	309	1	SCA3_TRIVA	P53401	trichomonas
846	5	3.7	290	1	KDSA_PEA	050044	pisum sativ	919	5	3.7	310	1	DP3B_MICLU	P21174	micrococcus
847	5	3.7	290	1	PARB_HELPJ	Q92K75	helicobacte	920	5	3.7	310	1	YCYJ_ECOLI	P76049	escherichia
848	5	3.7	290	1	PARB_HELPY	Q25758	helicobacte	921	5	3.7	311	1	E2B1_MERTH	Q27900	methanobact
849	5	3.7	290	1	RPOD_AERPE	Q9YDB3	aeropyrum p	922	5	3.7	311	1	PMG2_YEAST	Q12008	saccharomyc
850	5	3.7	290	1	SGCD_HUMAN	Q92629	homo sapien	923	5	3.7	312	1	MDH_ECOLI	P06994	escherichia
851	5	3.7	291	1	BLO1_KLEOX	P22391	klebsiella	924	5	3.7	312	1	MDH_SALTY	P25077	salmonella
852	5	3.7	291	1	MLER_LACIA	P16400	lactococcus	925	5	3.7	312	1	OGG1_MERTH	Q27337	methanobact
853	5	3.7	292	1	BIPI_TOBAC	003682	nicotiana t	926	5	3.7	312	1	TRXB_CHLMU	Q9PK47	chlamydia m
854	5	3.7	292	1	DAPA_ECO57	P58206	escherichia	927	5	3.7	312	1	TRXB_CHLTR	084101	chlamydia t
855	5	3.7	292	1	DAPA_ECOLI	P05640	escherichia	928	5	3.7	312	1	YTF1_ECO57	P58823	escherichia
856	5	3.7	292	1	GLMT_PIG	Q29555	sus scrofa	929	5	3.7	312	1	YTF1_ECOLI	P39317	escherichia
857	5	3.7	292	1	GLMT_RABIT	Q29513	oryctolagus	930	5	3.7	314	1	IF2A_HUMAN	P05198	homo sapien
858	5	3.7	292	1	GLMT_RAT	P13255	rattus norv	931	5	3.7	314	1	IF2A_RAT	P05199	rattus norv
859	5	3.7	292	1	SUCD_RICPR	008371	ricketsia	932	5	3.7	314	1	REP1_STRAU	P14490	staphylococ
860	5	3.7	292	1	YK14_YEAST	Q02202	saccharomyc	933	5	3.7	314	1	REP1_YEAST	004013	saccharomyc
861	5	3.7	293	1	BIPI_TOBAC	Q03686	nicotiana t	934	5	3.7	315	1	ATPG_STYPI	Q05384	synechococ
862	5	3.7	293	1	YD11_MERJA	Q58707	methanococc	935	5	3.7	315	1	CALU_HUMAN	Q43852	homo sapien
863	5	3.7	293	1	YNP7_CABEL	P34560	caenorhabdi	936	5	3.7	315	1	CALU_MOUSE	Q35887	mus musculus
864	5	3.7	294	1	DAPA_CAUCR	Q9A900	caulobacter	937	5	3.7	315	1	FHUD_BACSU	P37580	bacillus su
865	5	3.7	294	1	FBRL_TERTH	Q27200	tetrahymena	938	5	3.7	315	1	VN35_ROT11	Q03344	turkey rota
866	5	3.7	294	1	GLMT_HUMAN	Q14749	homo sapien	939	5	3.7	316	1	APBE_CHLTR	Q9PK42	chlamydia t
867	5	3.7	294	1	MP53_PHAQ	P56166	palatilis aq	940	5	3.7	316	1	APBE_CHLTR	084080	chlamydia t
868	5	3.7	295	1	GLUB_CORGL	P48242	corynebacte	941	5	3.7	316	1	BIA3_BACE	P06548	bacillus ce
869	5	3.7	295	1	LPXC_HELPJ	Q9ZM50	helicobacte	942	5	3.7	316	1	GBLP_NEUCR	Q01365	neurospora
870	5	3.7	295	1	YD64_MERJA	Q25692	helicobacte	943	5	3.7	316	1	PTA_RHIME	Q9X448	rhizobium m
871	5	3.7	295	1	Y234_MERJA	Q60258	methanococ	944	5	3.7	316	1	TAL_VIBCH	Q9KLW8	vibrio chol
872	5	3.7	296	1	SMDF_HUMAN	Q15491	homo sapien	945	5	3.7	316	1	YCZ0_YEAST	P25606	saccharomyc
873	5	3.7	297	1	LE33_CABEL	Q09581	caenorhabdi	946	5	3.7	316	1	YX12_CABEL	Q11123	caenorhabdi
874	5	3.7	297	1	PERR_ECOLI	Q57083	escherichia	947	5	3.7	317	1	APE_MACRA	P10517	macaca fasc
875	5	3.7	297	1	XLVA_BACSU	P39800	bacillus su	948	5	3.7	317	1	APE_PAPAN	P05770	papio anubi
876	5	3.7	297	1	YD67_MERJA	Q58762	methanococc	949	5	3.7	317	1	PIX2_HUMAN	Q99697	homo sapien
877	5	3.7	297	1	YIM4_YEAST	P40471	saccharomyc	950	5	3.7	317	1	PIX2_MOUSE	P17408	mus musculus
878	5	3.7	298	1	LAH1_SCHPO	P87058	schistosach	951	5	3.7	317	1	TLM_MOUSE	P66883	aquifex aeo
879	5	3.7	298	1	YN05_YEAST	P53843	saccharomyc	952	5	3.7	317	1	YC05_YEAST	P25616	saccharomyc
880	5	3.7	298	1	YN06_YEAST	P40167	saccharomyc	953	5	3.7	317	1	ACCA_ECOLI	P30867	escherichia
881	5	3.7	300	1	BLAB_PROVD	P52664	proteus vul	954	5	3.7	318	1	ATPS_YEAST	P24245	saccharomyc
882	5	3.7	300	1	YEO3_YEAST	Q69782	rhizobium m	955	5	3.7	318	1	MYOD_MOUSE	P10085	mus musculus
883	5	3.7	300	1	YE03_YEAST	P40035	saccharomyc	956	5	3.7	318	1	MYOD_MOUSE	Q02346	rattus norv
884	5	3.7	301	1	KIRN_BP14	P06855	bacterioph	957	5	3.7	318	1	MYOD_RAT	Q21325	desypus nov
885	5	3.7	301	1	YGBJ_HAETN	P44979	haemophilus	958	5	3.7	318	1	ND1M_DASNO	P66186	escherichia
886	5	3.7	302	1	RRM1_DROME	Q9VEPI	dirosophila	959	5	3.7	318	1	RSEB_ECOLI	P77324	escherichia
887	5	3.7	303	1	DDL_THEMA	P46805	thermotoga	960	5	3.7	318	1	YAGS_ECOLI	P77324	escherichia
888	5	3.7	303	1	DMA_TREPA	Q33844	treponema p	961	5	3.7	318	1	YJIA_ECOLI	P42403	escherichia
889	5	3.7	303	1	ROC_HUMAN	P07910	homo sapien	962	5	3.7	319	1	K6PF_THEMA	Q9WY52	thermotoga
890	5	3.7	304	1	BLAI_AERHY	Q44056	aeromonas h	963	5	3.7	319	1	MYOD_HUMAN	P15177	homo sapien
891	5	3.7	304	1	IGIR_PIG	Q29000	sus scrofa	964	5	3.7	319	1	MYOD_PIG	P49811	sus scrofa
892	5	3.7	304	1	INO2_YEAST	P26798	saccharomyc	965	5	3.7	319	1	MYOD_SHEEP	P29331	ovis aries
893	5	3.7	305	1	ILIVE_SYNY3	P54691	synechocyst	966	5	3.7	319	1	TERD_PSESP	P33010	pseudomonas
894	5	3.7	305	1	MIAA_AQUAE	O67162	aquifex aeo	967	5	3.7	320	1	ASPG_SPOFR	Q02467	spodoptera
895	5	3.7	305	1	PPX1_ARATH	P48528	arabidopsis	968	5	3.7	320	1	DIM1_KLULA	P78697	kluyveromyc
896	5	3.7	305	1	PPX2_ARATH	P48528	arabidopsis	969	5	3.7	320	1	FABG_CUPLA	P28645	cuphea lanc
897	5	3.7	305	1	YHCH_BACSU	P45492	bacillus su	970	5	3.7	320	1	HEM2_MERTC	Q02250	methanother
898	5	3.7	306	1	BLAC_BACAM	Q44674	bacillus am	971	5	3.7	320	1	LIPA_HAETN	P44463	haemophilus
899	5	3.7	306	1	BLAC_BACSU	P39824	bacillus su	972	5	3.7	320	1	VS10_TRTBB	P06012	typanosoma
900	5	3.7	307	1	BLAC_BACLI	P00808	bacillus li	973	5	3.7	320	1	YG11_YEAST	P33156	saccharomyc
901	5	3.7	307	1	COPE_CRIGR	O60445	criceulius	974	5	3.7	320	1	YNV5_YEAST	P40154	saccharomyc
902	5	3.7	307	1	KHSE_DEIRA	Q98895	delinococcus	975	5	3.7	321	1	AOX1_SOYBN	Q07185	glycine max
903	5	3.7	307	1	MMP1_MYCAV	Q48899	mycobacteri	976	5	3.7	321	1	YWJ1_BACSU	Q03224	bacillus su
904	5	3.7	307	1	MMP1_MYCLE	P46841	mycobacteri	977	5	3.7	322	1	ARCG_ANNAP	P54894	anabena sp
905	5	3.7	307	1	QOX2_ACAC	P50653	acetobacter	978	5	3.7	322	1	COAT_RSVT	P26657	rice stripe
906	5	3.7	307	1	UFDI_MOUSE	P70362	mus musculus	979	5	3.7	322	1	COO3_ARATH	Q49354	a hexapreny
907	5	3.7	307	1	VP53_BPAPS	Q91157	bacterioph	980	5	3.7	322	1	PTA_MYCCA	Q49157	mycoplasma
908	5	3.7	308	1	ABCA_AERSA	Q07698	aeromonas s	981	5	3.7	322	1	ADAX_BACSU	P34952	bacillus su
909	5	3.7	308	1	METE_MERTU	Q58866	methanococc	982	5	3.7	322	1	RADA_MERTU	Q73948	methanococc

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983 5 3.7 322 1 SLPI_DROME P32030 drosophila
984 5 3.7 322 1 TRXB_SCHPO Q92375 schizosacch
985 5 3.7 323 1 CRO_RANCA P17264 rana catesb
986 5 3.7 323 1 CRO_RANTE P02532 rana tempor
987 5 3.7 323 1 G731_HUMAN P09758 homo sapien
988 5 3.7 323 1 PIMI_XENLA Q91822 xenopus lae
989 5 3.7 323 1 PREA_CYACA Q91811 cyano didium c
990 5 3.7 324 1 E2B2_PYPAB Q9V281 pyrococcus
991 5 3.7 324 1 I12B_PIG Q28938 sus scrofa
992 5 3.7 324 1 Y700_METJA Q58111 methanococ
993 5 3.7 324 1 YB1_HUMAN P16991 homo sapien
994 5 3.7 324 1 YF02_METJA Q58897 methanococ
995 5 3.7 326 1 UNG2_HUMAN P22674 homo sapien
996 5 3.7 326 1 Y0B0_BACSU P45950 bacillus su
997 5 3.7 327 1 EBGR_ECOLI P06846 escherichia
998 5 3.7 327 1 FBRL_GIALA Q24957 giardia lam
999 5 3.7 327 1 FBRL_YEAST P15646 saccharomyc
1000 5 3.7 327 1 I12B_BOVIN P46282 bos taurus

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ALIGNMENTS

RESULT 1

SAK_STAAU STANDARD: PRT: 163 AA.

AC P00802; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III).
 GN SAK.

OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;

RP SEQUENCE FROM N.A.
 RX MEDLINE=84069795; PubMed=6359061;
 RA Sako T., Tsuchida N.;

RT "Nucleotide sequence of the staphylokinase gene from Staphylococcus
 aureus.";
 RL Nucleic Acids Res. 11:7679-7693(1983).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 43-163.
 RX MEDLINE=97290447; PubMed=9145104;
 RA Rabijs A., de Bondt H.L., de Kanter C.;

RT "Three-dimensional structure of staphylokinase, a plasminogen
 activator with therapeutic potential.";
 RL Nat. Struct. Biol. 4:357-360(1997).
 RN [3]

RP STRUCTURE BY NMR OF 28-163.
 RX MEDLINE=96367505; PubMed=9692953;
 RA Ohlenschlaeger O., Ramachandran R., Guehrs K.H., Schloft B.,
 RA Brown L.R.;

RT "Nuclear magnetic resonance solution structure of the plasminogen-
 activator protein staphylokinase.";
 RL Biochemistry 37:10635-10642(1998).
 RN [1]

CC -!- FUNCTION: THIS EXTRACELLULAR PROTEIN IS ONE OF THE PLASMINOGEN
 ACTIVATORS THAT CONVERTS PLASMINOGEN INTO PLASMIN. IT REQUIRES
 CALCIUM ION FOR STABILIZATION.

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DR EMBL; X00127; CAA24957.1; -;
 DR PIR; A00995; PRSAK.
 DR PDB; 2SAK; 25-FEB-98.

DR PDB; 1SSN; 02-DEC-98.
 KW Hydrolyase; Calcium; Plasminogen activation; Signal; 3D-structure.
 FT SIGNAL 1
 FT CHAIN 28 163
 SQ SEQUENCE 163 AA; 18490 MW; E5609F50ADE141 CRC64;

Query Match 75.0%; Score 102; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1,4e-97;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 KGNELISPHYVEPIKPGTTLKEKIEYVEMALDFAKERRVVELDPSAKIEVYYDK 94
 DB 62 KGNELISPHYVEPIKPGTTLKEKIEYVEMALDFAKERRVVELDPSAKIEVYYDK 121
 QY 95 NKKKEETKSPITEKGFVVDLSEHIKNPGLITKVIEKK 136
 DB 122 NKKKEETKSPITEKGFVVDLSEHIKNPGLITKVIEKK 163

RESULT 2

SAK_BPP42 STANDARD: PRT: 163 AA.

AC P15240; 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III).
 GN SAK.

OS Bacteriophage P42D.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 OX NCBI_TaxID=10715;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88121731; PubMed=3123893;
 RA Behnke D., Gerlach D.;

RT "Cloning and expression in Escherichia coli, Bacillus subtilis, and
 RT Streptococcus sanguis of a gene for staphylokinase -- a bacterial
 RT plasminogen activator.";
 RL Mol. Gen. Genet. 210:528-534(1987).
 RN [1]

CC -!- FUNCTION: THIS EXTRACELLULAR PROTEIN IS ONE OF THE PLASMINOGEN
 ACTIVATORS THAT CONVERTS PLASMINOGEN INTO PLASMIN. IT REQUIRES
 CALCIUM ION FOR STABILIZATION.

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DR EMBL; X06603; CAA29822.1; -;
 DR EMBL; M57455; AA98206.1; -;
 DR EMBL; A17537; CAA01341.1; -;
 DR PIR; S02330; S02330.
 DR HSSP; P00802; 2SAK.

RT Hydrolyase; Calcium; Plasminogen activation; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 163
 FT SIGNAL 27
 FT CHAIN 28 163

SO SEQUENCE 163 AA; 18608 MW; AA267A4FF75D36EC CRC64;

Query Match 68.4%; Score 93; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2,6e-88;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEPIKPGTTLKEKIEYVEMALDFAKERRVVELDPSAKIEVYYDKNKKKEETKS 103
 DB 71 YVEPIKPGTTLKEKIEYVEMALDFAKERRVVELDPSAKIEVYYDKNKKKEETKS 130
 QY 104 FPITEKGFVVDLSEHIKNPGLITKVIEKK 136

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DB 131 PPTKEGVVVDLSEHINKNFNLITKVLKK 163
|||||
RESULT 3
TRPA_HALN1 STANDARD; PRT; 204 AA.
AC Q9H8B9;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE TRYPHOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20).
GN TRPA OR VNG0308G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_Taxid=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahatras G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Iendbarger T.A., Peck R.F., Fohlischroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
CC OF INDOLGLYCEROL PHOSPHATE TO INDOL AND GLYCERALDEHYDE 3-
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: L-SERINE + L-(INDOL-3-YL)GLYCEROL 3-PHOSPHATE
CC = L-TRYPTOPHAN + GLYCERALDEHYDE 3-PHOSPHATE + H(2)O.
CC -1- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TRIMER OF TWO ALPHA AND TWO BETA CHAINS (BY
CC SIMILARITY). BELONGS TO THE TRPA FAMILY.
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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CC -----
DR EMBL: AE004991; AAC18888.1; -
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR003028; TRP_synthase_alpha.
DR Pfam: PF00290; trp_synta.1.
DR ProDom: PD001535; TRP_synthase_alpha.1.
DR ProSite: PS00167; TRP_SYNTHASE_ALPHA; FALSE NEG.
DR Trypophan biosynthesis; lyase, complete proteome.
KW SEQUENCE 204 AA; 21172 MW; 7723CC4483A5ED0C CRC64;
SQ
Query Match 5.1%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 110 GFWVPDL 116
Db 51 GFWVPDL 57
|||||
RESULT 4
CTRA_CAUCR STANDARD; PRT; 231 AA.
ID 045994;
AC 045994;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DB 131 PPTKEGVVVDLSEHINKNFNLITKVLKK 163
|||||
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CELL CYCLE TRANSCRIPTIONAL REGULATOR CTRA (RESPONSE REGULATOR SOKA).
GN CTRA OR SOKA OR CC3035.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_Taxid=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB15N / NA1000;
RX MEDLINE=96140642; PubMed=8548829;
RA Ohn K.C., Marcynski G.T., Shapiro L.;
RT "cell cycle control by an essential bacterial two-component signal
RT transduction protein."
RL Cell 84:83-93(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Delonay J.F., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kohnen J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Yamathayan J., Ermolaeva M., White O.,
RA Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [3]
RP SEQUENCE OF 159-231 FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=98132609; PubMed=9465034;
RA Wu J., Ohta N., Newton A.;
RT "An essential, multicomponent signal transduction pathway required for
RT cell cycle regulation in Caulobacter."
RL Proc. Natl. Acad. Sci. U.S.A. 95:1443-1448(1998).
CC -1- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC CTRA/CCRA THAT CONTROLS MULTIPLE EVENTS IN THE CELL CYCLE,
CC INCLUDING CELL DIVISION, STALK SYNTHESIS, AND CELL CYCLE-SPECIFIC
CC TRANSCRIPTION. BINDS TO A GROUP OF CELL CYCLE-REGULATED PROMOTERS
CC CRITICAL FOR DNA REPLICATION, DNA METHYLATION, AND CLASS II
CC FLAGELLAR BIOGENESIS.
CC -1- PTM: PHOSPHORYLATED BY CCKA.
CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -----
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CC -----
DR EMBL: U39559; AAA93080.1; -
DR EMBL: AE005966; AAK24997.1; -
DR EMBL: AF021339; AAC05479.1; -
DR TIGR: CC3035; -
DR InterPro: IPR001789; Trans_reg.
DR InterPro: IPR001867; Trans_reg.C.
DR Pfam: PF00072; response_reg.1.
DR Pfam: PF00486; trans_reg.C.1.
DR SMART: SM00448; REC.1.
DR Sensory transduction; Phosphorylation; Transcription regulation;
KW DNA-binding; complete proteome.
FT MOD_RES 51 51 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25796 MW; BB812AF6DADAB8 CRC64;
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QY 52 GTTITKE 58
GN 1111111
DB 166 GTTITKE 172

RESULT 5
TRPA_HALVO STANDARD: PRT; 277 AA.
ID TRPA_HALVO
AC P18284;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20).
GN TRPA.
OS Halobacterium volcanii (Halobacter volcanii).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
OX NCBI_TaxID=2246;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370836; PubMed=2118654;
RA Lam W.L., Cohen A., Tsoulfas D., Doolittle W.F.;
RT "Genes for tryptophan biosynthesis in the archaeobacterium Haloferax
RT volcanii."
RT Proc. Natl. Acad. Sci. U.S.A. 87:6614-6618(1990).
CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
CC OF INDOLBUTYRYL PHOSPHATE TO INDOL AND GLYCERALDEHYDE 3-
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: L-SERINE + L-(INDOL-3-YL)GLYCEROL 3-PHOSPHATE
CC = L-TRYPTOPHAN + GLYCERALDEHYDE 3-PHOSPHATE + H(2)O.
CC -1- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
-----
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-----
DR EMBL: M36177; AAA72864.1; -.
DR PIR: A36044; A36044.
DR HSSP: P00929; 1BKS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR002028; TRP_synthase_alpha.
DR Pfam: PF00290; trp_syna. 1.
DR ProDom: PD001535; TRP_synthase_alpha; 1.
DR PROSITE: PS00167; TRP_SYNTHASE_ALPHA; 1.
KW Tryptophan biosynthesis; Lyase.
FT ACT_SITE 54 54 INVOLVED IN PROTON DONATION/ACCEPRATION
FT BINDING 205 208 DURING CATALYSIS.
FT FT SUBSTRATE.
SQ SEQUENCE 277 AA; 29720 MW; 22F68CE6826B0E61 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GFVVPDL 116
GN 1111111
DB 120 GFVVPDL 126

RESULT 6
TRXB_NEUCR STANDARD: PRT; 334 AA.
ID TRXB_NEUCR
AC P51978;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

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DE THIOREDOXIN REDUCTASE (EC 1.6.4.5).
GN CYS-9.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACR-2;
RA Onai K., Takayanagi K., Nakashima H.;
RT Submitted (Apr-1985) to the EMBL/Genbank/DDJ databases.
CC -1- CATALYTIC ACTIVITY: NADPH + OXIDIZED THIOREDOXIN = NADP(+) +
CC REDUCED THIOREDOXIN.
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
CC OXIDOREDUCTASES CLASS-II.
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DR EMBL: D45049; BAA08090.1; -.
DR HSSP: Q39243; 1VDC.
DR InterPro: IPR001327; FAD_Pyr_redox.
DR InterPro: IPR00103; Pyridine_redox_2.
DR Pfam: PF00070; Pyr_redox; 1.
DR PRINTS: PR00368; FADPNR.
DR PROSITE: PR00469; PNDPRTASEII.
DR PROSITE: PS00573; PYRIDINE_REDOX_2; 1.
KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
FT NP_BIND 7 24 FAD (ADP PART) (PROBABLE).
FT DISULFID 140 143 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 155 168 NAD(P) (BY SIMILARITY).
FT NP_BIND 277 309 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 334 AA; 35882 MW; 4D9E9861E479EB4 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 KPCTILT 56
GN 1111111
DB 271 KPCTILT 277

RESULT 7
PBPL_YEAST STANDARD: PRT; 722 AA.
ID PBPL_YEAST
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PBPL-RINDING PROTEIN 1.
GN PBPL OR WR516 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Hedling U., Holmann B., Delius H.;
RT Submitted (May-1996) to the EMBL/Genbank/DDJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=DBY747;

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RA Mecklenbrauker I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns.";
RL Theiss (1996), Vienna Biocentre, Austria.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=99038243; Pubmed=9819425;
RA Mangus D.A., Amrani N., Jacobson A.;
RT "Pbplp, a factor interacting with Saccharomyces cerevisiae poly(A)-
RT binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998)
CC -1- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PBPLP, THE 3' TERMINI OF PRE-MRNAs ARE PROPERLY CLEAVED
CC OR PBPLP TO NEGATIVELY REGULATE POLYADENYLATION.
CC -1- SUBUNIT: INTERACTS WITH PAB1.
CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -----
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CC -----
DR EMBL; Z72963; CA97204.1; -
DR EMBL; U46931; AAB94294.1; -
DR SGD; S0003410; PBPL.
KW Nuclear protein.
SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 1; Length 722;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KKGDAS 16
    |||||
Db 514 KKGDAS 520

RESULT 8
IF2_HELPY STANDARD; PRT; 944 AA.
ID IF2_HELPY
AC P55972;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSLATION INITIATION FACTOR IF-2.
GN INFB OR HP1048.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; Pubmed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McEwen K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Kap P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -1- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION

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CC OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORMYL-METHIONYL-tRNA FROM
CC SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S
CC RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
CC DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
CC -----
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CC -----
DR EMBL; AE000612; AAD08093.1; -
DR HSSP; P02990; IEFU.
DR TIGR; HP1048; -
DR InterPro; IPR000795; GTP_EFTU.
DR InterPro; IPR00178; IF2.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF02131; IF2; 1.
DR ProDom; PD186100; IF2; 1.
DR PROSITE; PS01176; IF2; 1.
KW Initiation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT DOMAIN 446 594 G-DOMAIN.
FT NP_BIND 452 459 GTP (BY SIMILARITY).
FT NP_BIND 498 502 GTP (BY SIMILARITY).
FT NP_BIND 552 555 GTP (BY SIMILARITY).
SQ SEQUENCE 944 AA; 105194 MW; EC90404D9C3B851D CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 1; Length 944;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KKEETKS 103
    |||||
Db 96 KKEETKS 102

RESULT 9
POL_HV2CA STANDARD; PRT; 1034 AA.
ID POL_HV2CA
AC P24107;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL POLYPEPTIDE [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 2 (isolate CAM2) (HIV-2).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11715;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91170959; Pubmed=2005437;
RT "Nucleotide sequence of a Guinea-Bissau-derived human
RT J. Gen. Virol. 72:721-724(1991).
RL -1- PWM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR TGA MAY OCCUR BETWEEN
CC 564-ILE AND 565-GLY.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC PIR; B38475; GNJCJA.
CC HSSP; P04584; IJLD.
DR MEROPS; A02.002; -
DR InterPro; IPR001995; Asp_prot_retrov.
DR InterPro; IPR001969; Asp_protease.

```

DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_zn.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00552; Integrase_1.
DR Pfam: PF02022; Integrase_zn; 1.
DR Pfam: PF00075; RNaseH; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS0175; ASP_PROT_RETROV; 1.
DR AIDS: Polypotein; Hydrolyase; Aspartyl protease; Endonuclease;
KM Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 85 183
FT ACT SITE 109 109 BY SIMILARITY.
SO SEQUENCE 1034 AA; 117195 MW; 3514E566AA6D7C86 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 1034;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LTRKIE 61
DB 209 LTRKIE 215

RESULT 10
POL_HV2KR STANDARD; PRT; 1035 AA.
ID 074120;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
NCBI_TaxID=73484;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G.K., Talbot R., Leavitt M., Luznick L., Schmidt A.,
RL Badel P., Barz C., Morton W., Wong-Scaal F., Looney D.J.;
Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
CC -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U22047; AAA64576.1; -.
DR HSSP: P04584; IJLD.
DR InterPro: IPR001995; Asp_prot_retrov.
DR InterPro: IPR001969; Asp_protease.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_zn.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF02022; Integrase_zn; 1.
DR Pfam: PF00075; RNaseH; 1.
DR Pfam: PF00665; rve; 1.

DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS0175; ASP_PROT_RETROV; 1.
DR AIDS: Polypotein; Hydrolyase; Aspartyl protease; Endonuclease;
KM Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 85 183
FT ACT SITE 109 109 BY SIMILARITY.
SO SEQUENCE 1035 AA; 117632 MW; 696EDC6CAFBD06CF CRC64;

Query Match 5.1%; Score 7; DB 1; Length 1035;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LTRKIE 61
DB 209 LTRKIE 215

RESULT 11
POL_HV2NZ STANDARD; PRT; 1035 AA.
ID AC P05962; Q85571;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
NCBI_TaxID=11719;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88320359; PubMed=3261862;
RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R.,
RA Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F.,
RA Arya S.K., Josephs S.F., Zagury D., Wong-Straal F., Gallo R.C.;
RT "Genetic variability between isolates of human immunodeficiency virus
RT (HIV) type 2 is comparable to the variability among HIV type 1";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
CC -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03654; AAB0075.1; ALT_INIT.
DR HSSP: P04584; IJLD.
DR HIV: J03654; POLS2NIHZ.
DR MEROPS: A02.002; -.
DR InterPro: IPR001995; Asp_prot_retrov.
DR InterPro: IPR001969; Asp_protease.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_zn.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF02022; Integrase_zn; 1.
DR Pfam: PF00075; RNaseH; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; FALSE_NEG.

DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
FT CHAIN 85 183
FT ACT_SITE 109 109
SQ SEQUENCE 1035 AA; 117323 MW; E3DC4E2DF457F6BA CRC64;
BY SIMILARITY.
Query Match 5.1%; Score 7; DB 1; Length 1035;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 LTRKIE 61
DB 209 LTRKIE 215
RESULT 12
POL_HV2RO STANDARD; PRT; 1036 AA.
ID POL_HV2RO
AC P04584; Q76629;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
GN POL.
OS Human immunodeficiency virus type 2 (Isolate ROD) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87173056; PubMed=3031510;
RA Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,
RA Alizon M.;
RT "Genome organization and transactivation of the human
RT immunodeficiency virus type 2.";
RL Nature 326:662-669(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-184.
RX MEDLINE=93391360; PubMed=8378311;
RA Tong L., Pav S., Pargellis C., Do F., Lamarre D., Anderson P.C.;
RT "Crystal structure of human immunodeficiency virus (HIV) type 2
RT protease in complex with a reduced amide inhibitor and comparison
RT with HIV-1 protease structures.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8387-8391(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-184 IN COMPLEX WITH INHIB.
RX MEDLINE=95014470; PubMed=7929352;
RA Chen Z., Li Y., Chen E., Hall D.L., Darke P.L., Culbertson C.,
RA Shafer J.A., Kuo L.C.;
RT "Crystal structure at 1.9-A resolution of human immunodeficiency
RT virus (HIV) II protease complexed with L-735,524, an orally
RT bioavailable inhibitor of the HIV proteases.";
RL J. Biol. Chem. 269:26344-26348(1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-184 IN COMPLEX WITH INHIB.
RX MEDLINE=95338600; PubMed=7613867;
RA Priestle J.P., Fessler A., Rosel J., Tintelnot-Blomley M., Strop P.,
RA Grutter M.G.;
RT "Comparative analysis of the X-ray structures of HIV-1 and HIV-2
RT proteases in complex with CGP 53820, a novel pseudosymmetric
RT inhibitor.";
RL Structure 3:381-389(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 86-184 IN COMPLEX WITH INHIB.
RX MEDLINE=97359919; PubMed=9216835;
RA Beaulieu P.L., Wernic D., Abraham A., Anderson P.C., Bogri T.,
RA Bousquet Y., Croteau G., Guse I., Lamarre D., Lhard F., Paris W.,
RA Thibault D., Pav S., Tong L.;
RT "Potent HIV protease inhibitors containing a novel
RT (hydroxyethyl)amide isostere.";
RL J. Med. Chem. 40:2164-2176(1997).

CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
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CC -----
CC EMBL; M15390; -; NOT_ANNOTATED_CDS.
CC EMBL; X05291; -; NOT_ANNOTATED_CDS.
CC EMBL; M15390; AAB00764.1; ALT_INIT.
CC PIR; B26262; GN.LG2.
CC DR PDB; 1PHV; 15-OCT-94.
CC DR PDB; 2PHV; 15-OCT-94.
CC DR PDB; 2MIP; 15-APR-92.
CC DR PDB; 2HPE; 15-OCT-94.
CC DR PDB; 2HPE; 15-OCT-94.
CC DR PDB; 1HIT; 10-JUL-95.
CC DR PDB; 1HST; 03-APR-96.
CC DR PDB; 1HST; 03-APR-96.
CC DR PDB; 1HST; 26-JAN-95.
CC DR PDB; 1HST; 26-JAN-95.
CC DR PDB; 1HST; 03-DEC-97.
CC DR PDB; 3UPJ; 14-OCT-96.
CC DR PDB; 4UPJ; 14-OCT-96.
CC DR PDB; 5UPJ; 21-APR-97.
CC DR PDB; 6UPJ; 21-APR-97.
CC DR HIV; M15390; POL52ROD.
CC DR MEROPS; A02.002; -;
CC DR InterPro; IPR001995; Asp_prol_retrov.
CC DR InterPro; IPR001969; Asp_protease.
CC DR InterPro; IPR001037; Integrase_C.
CC DR InterPro; IPR003308; Integrase_zn.
CC DR InterPro; IPR002156; RNaseH.
CC DR InterPro; IPR00477; RNaseH.
CC DR Pfam; PF00552; Integrase_1.
CC DR Pfam; PF02022; Integrase_zn; 1.
CC DR Pfam; PF00075; RNaseH; 1.
CC DR Pfam; PF00665; IVE; 1.
CC DR Pfam; PF00077; IVP; 1.
CC DR Pfam; PF00078; IVP; 1.
CC DR PROSITE; PS00141; ASP_PROTEASE; 1.
CC DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
FT CHAIN 86 184
FT ACT_SITE 110 110
SQ SEQUENCE 1036 AA; 117080 MW; 5224E354B1DCC83B CRC64;
BY SIMILARITY.
FT STRAND 87 89
FT STRAND 95 100
FT TURN 101 102
FT STRAND 103 109
FT TURN 111 112
FT STRAND 117 118
FT STRAND 128 134
FT STRAND 138 151
FT TURN 152 153
FT STRAND 154 162
FT STRAND 169 170
FT HELIX 172 178
FT TURN 179 179
FT STRAND 181 183
FT STRAND 181 183
Query Match 5.1%; Score 7; DB 1; Length 1036;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LTKERIE 61
|||||
Db 210 LTKERIE 216

RESULT 13
POL_HV2G1 STANDARD: PRT; 1049 AA.
AC P18042;
DT 01-FEB-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11717;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90112350; PubMed=2611042;
RA Hasegawa A., Tsujimoto H., Maki N., Ishikawa K.I., Miura T.,
RA Fukusawa M., Miki K., Hayami M.,
RT "Genomic divergence of HIV-2 from Ghana."
RL AIDS Res. Hum. Retroviruses 5:593-604(1989).
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
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CC -----
CC EMBL; M30895; AAA43933.1; -
DR PIR; J50328; GNLJGG.
DR HSSP; P04584; 1JUD.
DR HIV; M30895; POLS2GHL.
DR MEROPS; A02.002. -
DR InterPro; IPR001995; Asp_prot_retrov.
DR InterPro; IPR001969; Asp_protease.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_zn.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR001584; Rve.
DR Pfam; PF00552; Integrase_1.
DR Pfam; PF02022; Integrase_zn; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
DR AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 98 207
FT ACT_SITE 123 123 BY SIMILARITY.
SQ SEQUENCE 1049 AA; 119087 MW; D0123D490E899FC3 CRC64;

QY 55 LTKERIE 61
|||||
Db 223 LTKERIE 229

Query Match 5.1%; Score 7; DB 1; Length 1049;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
POL_HV2ST STANDARD: PRT; 1055 AA.
AC P20876;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 2 (isolate ST) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11721;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90112662; PubMed=2296086;
RA Kumar P., Hui H., Kappes J.C., Hagarty B.S., Hoxie J.A., Arya S.K.,
RA Shaw G.M., Hahn B.H.;
RT "Molecular characterization of an attenuated human immunodeficiency
RT virus type 2 isolate."
RL J. Virol. 64:890-901(1990).
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
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CC -----
CC EMBL; M31113; -; NOT_ANNOTATED_CDS.
DR PIR; B33943; GNLJST.
DR HSSP; P04584; 1JUD.
DR HIV; M31113; POLS2ST.
DR MEROPS; A02.002. -
DR InterPro; IPR001995; Asp_prot_retrov.
DR InterPro; IPR001969; Asp_protease.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_zn.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR001584; Rve.
DR Pfam; PF00552; Integrase_1.
DR Pfam; PF02022; Integrase_zn; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
DR AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 105 203
FT ACT_SITE 129 129 BY SIMILARITY.
SQ SEQUENCE 1055 AA; 119767 MW; A943310E567889B1 CRC64;

QY 55 LTKERIE 61
|||||
Db 229 LTKERIE 235

Query Match 5.1%; Score 7; DB 1; Length 1055;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

POL_HV2D1
ID POL_HV2D1 STANDARD; PRT; 1073 AA.
AC P1757;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
GN POL.
OS Human immunodeficiency virus type 2 (isolate D194) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11713;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184631; PubMed=2467304;
RA Kuehnelt H., Kreutz R., Ruesamen-Waigmann H., Mix D.,
Blesert L., Kreutz R., Immelman A., Henco K., Melchsner C.,
Andreesen R., Gelderblom H., Ruesamen-Waigmann H.;
RT "Molecular cloning of two west African human immunodeficiency virus
type 2 isolates that replicate well in macrophages: a Gambian
isolate, from a patient with neurologic acquired immunodeficiency
syndrome, and a highly divergent Ghanaian isolate."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045094; PubMed=2235509;
RA Kuehnelt H., Kreutz R., Ruesamen-Waigmann H.;
RT "Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of
'neuro-AIDS', which showed excellent growth in macrophages."
RL Nucleic Acids Res. 18:6142-6142(1990).
CC -I- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
CC -I- MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF
'NEURO-AIDS'.
CC -I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
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CC -----
DR EMBL; J04542; AAA76841.2; -;
DR EMBL; X52223; -; NOT_ANNOTATED_CDS.
DR PIR; S12153; S12153.
DR HSSP; P04584; 1TLD.
DR HIV; J04542; POL52D194.
DR MEROPS; A02.002; -;
DR InterPro; IPR001995; Asp_prol_retrov.
DR InterPro; IPR001969; Asp_protease.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_zn.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase_1.
DR Pfam; PF02022; Integrase_2n; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 123 221
FT ACT_SITE 147 147
FT BY_SIMILARITY PROTEASE (BY SIMILARITY).
SQ SEQUENCE 1073 AA; 121071 MW; B3AA099483B4B3CF CRC64;

Query Match 5.18; Score 7; DB 1; Length 1073;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LTKKIE 61
DB 247 LTKKIE 253

Search completed: April 22, 2002, 10:49:02
Job time: 197 sec

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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:45:25 ; Search time 24.86 Seconds
(without alignments)
800.203 Million cell updates/sec

Title: US-09-601-490-1

Perfect score: 136
Sequence: 1 SSSFDKGGKKKGDSAYFEP.....SEHKPGFNLTQVIEKK 136Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: SPREMBL.17:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_Mhc:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	100.0	163	2	099SU7
2	100	73.5	136	2	033929
3	97	71.3	163	2	09LC46
4	93	68.4	163	2	09AM04
5	8	5.9	245	2	09X260
6	7	5.1	56	1	027388
7	7	5.1	90	6	028835
8	7	5.1	92	12	086603
9	7	5.1	102	2	09K8J5
10	7	5.1	114	12	09JEH2
11	7	5.1	138	2	09KEP3
12	7	5.1	140	12	09OU35
13	7	5.1	154	12	09RT01
14	7	5.1	181	5	09NE98
15	7	5.1	185	2	09ACCO
16	7	5.1	194	2	084552
17	7	5.1	219	5	045975
18	7	5.1	221	12	09IVA8
19	7	5.1	224	12	098X05

20	7	5.1	224	12	098BW5	098w5 human immun
21	7	5.1	232	2	09ZHS1	09ZHS1 Brucella ab
22	7	5.1	233	2	09FD95	09FD95 Rhizobium m
23	7	5.1	236	12	090226	090226 turnip mosa
24	7	5.1	237	2	09RNH4	09RNH4 rhodobacter
25	7	5.1	250	12	0991V8	0991V8 human immun
26	7	5.1	263	10	09MSK7	09MSK7 glycine max
27	7	5.1	276	10	09SG92	09SG92 arabidopsis
28	7	5.1	288	12	088917	088917 turnip mosa
29	7	5.1	288	12	088599	088599 turnip mosa
30	7	5.1	288	12	P89215	P89215 turnip mosa
31	7	5.1	288	12	09IC16	09IC16 turnip mosa
32	7	5.1	288	12	09IC15	09IC15 turnip mosa
33	7	5.1	288	12	09IC14	09IC14 turnip mosa
34	7	5.1	288	12	09DKY5	09DKY5 turnip mosa
35	7	5.1	288	12	099DD0	099DD0 turnip mosa
36	7	5.1	288	12	099DC9	099DC9 turnip mosa
37	7	5.1	288	12	099PC8	099PC8 turnip mosa
38	7	5.1	298	12	09WA68	09WA68 turnip mosa
39	7	5.1	298	12	09WA67	09WA67 turnip mosa
40	7	5.1	298	12	09WA66	09WA66 turnip mosa
41	7	5.1	298	12	09WA64	09WA64 turnip mosa
42	7	5.1	298	12	09WA63	09WA63 turnip mosa
43	7	5.1	298	12	09WA62	09WA62 turnip mosa
44	7	5.1	298	12	09WA61	09WA61 turnip mosa
45	7	5.1	303	13	09IB66	09IB66 xenopus lae
46	7	5.1	311	2	09KET0	09KET0 bacillus ha
47	7	5.1	332	2	09XDU2	09XDU2 clostridium
48	7	5.1	341	12	09BWR7	09BWR7 human immun
49	7	5.1	343	1	09YDE0	09YDE0 aeropyrum p
50	7	5.1	343	12	09J5A2	09J5A2 fowlpox vir
51	7	5.1	349	12	09EAK0	09EAK0 human immun
52	7	5.1	351	12	09E3T6	09E3T6 human immun
53	7	5.1	351	12	09E3T5	09E3T5 human immun
54	7	5.1	351	12	09E3T4	09E3T4 human immun
55	7	5.1	351	12	09E3T3	09E3T3 human immun
56	7	5.1	351	12	09E3T2	09E3T2 human immun
57	7	5.1	351	12	09E3T1	09E3T1 human immun
58	7	5.1	353	12	09IGK4	09IGK4 human immun
59	7	5.1	361	12	099EM9	099EM9 turnip mosa
60	7	5.1	361	12	099EM8	099EM8 turnip mosa
61	7	5.1	361	12	099EM7	099EM7 turnip mosa
62	7	5.1	370	2	09KZV9	09KZV9 streptomyce
63	7	5.1	371	2	09KFO8	09KFO8 bacillus ha
64	7	5.1	374	2	09LC69	09LC69 bacillus su
65	7	5.1	379	12	070792	070792 calanthe m
66	7	5.1	381	10	09SEV5	09SEV5 gulliardia
67	7	5.1	391	12	098Y20	098Y20 human immun
68	7	5.1	398	2	09WZL9	09WZL9 thermotoga
69	7	5.1	399	5	044999	044999 caenorhabdi
70	7	5.1	405	12	088563	088563 turnip mosa
71	7	5.1	408	12	099251	099251 turnip yell
72	7	5.1	449	5	020198	020198 caenorhabdi
73	7	5.1	476	12	09PYR0	09PYR0 human immun
74	7	5.1	492	12	09PYR9	09PYR9 turnip mosa
75	7	5.1	497	12	099K04	099K04 turnip mosa
76	7	5.1	499	12	09IC19	09IC19 turnip mosa
77	7	5.1	499	12	09IC18	09IC18 turnip mosa
78	7	5.1	499	12	09EAA9	09EAA9 turnip mosa
79	7	5.1	499	12	0998R4	0998R4 turnip mosa
80	7	5.1	560	12	006347	006347 human immun
81	7	5.1	563	12	09Q8G8	09Q8G8 myxoma viru
82	7	5.1	589	12	09DII9	09DII9 human immun
83	7	5.1	598	12	09DII6	09DII6 human immun
84	7	5.1	694	1	09V0H3	09V0H3 pyrococcus
85	7	5.1	721	2	086171	086171 clostridium
86	7	5.1	801	12	041344	041344 turnip mosa
87	7	5.1	999	12	090082	090082 human immun
88	7	5.1	999	12	090099	090099 human immun
89	7	5.1	1008	5	077391	077391 plasmodium
90	7	5.1	1035	12	073194	073194 human immun
91	7	5.1	1055	12	09YRU0	09YRU0 human immun
92	7	5.1	1059	12	076630	076630 human immun

93	7	5.1	1188	4	Q9H288	Q9H288 homo sapien	166	6	4.4	219	13	Q9370	Q9370 gallus gall
94	7	5.1	1599	11	Q99NH0	Q99nh0 mus musculu	167	6	4.4	226	2	Q9KBX0	Q9bX0 bacillus na
95	7	5.1	3164	12	Q9IC12	Q9ic12 tunip mosa	168	6	4.4	226	11	Q9JLX3	Q9jlx3 rattus norv
96	6	4.4	21	6	Q9TR36	Q9tr36 bos taurus	169	6	4.4	227	3	Q59775	Q59775 schizosacch
97	6	4.4	72	11	P97850	P97850 rattus norv	170	6	4.4	227	5	Q9V4C7	Q9v4c7
98	6	4.4	77	2	Q9JWU8	Q9jwU8 neisseria m	171	6	4.4	227	10	Q9FUS9	Q9fU9 arabisopilla
99	6	4.4	80	2	Q9KW25	Q9Kw25 xanthomonas	172	6	4.4	227	10	Q9FES8	Q9fE8 lycopersico
100	6	4.4	85	2	Q9WVG1	Q9wvg1 xanthomonas	173	6	4.4	230	2	Q9Z5A2	Q9z5a2 streptomyc
101	6	4.4	89	1	Q9BJR9	Q9bjr9 thermoplasma	174	6	4.4	230	11	Q9JKB1	Q9jkb1 mus musculu
102	6	4.4	90	1	Q9HJR9	Q9hjr9 thermoplasma	175	6	4.4	230	11	Q9EOX7	Q9eox7 mus musculu
103	6	4.4	93	3	Q12497	Q12497 saccharomyc	176	6	4.4	230	13	Q9P6C7	Q9p6c7 gallus gall
104	6	4.4	100	3	P87070	P87070 laccaria bi	177	6	4.4	231	2	Q509P7	Q509p7 borrelia bu
105	6	4.4	103	5	Q15656	Q15656 plasmodium	178	6	4.4	231	2	Q9QX6	Q9qX6 neisseria m
106	6	4.4	111	2	Q9S085	Q9s085 borrelia bu	179	6	4.4	231	2	Q9JPK0	Q9jpk0 neisseria m
107	6	4.4	111	2	Q06696	Q06696 borrelia bu	180	6	4.4	231	2	Q9JPU9	Q9jpu9 neisseria m
108	6	4.4	112	2	Q9FLL1	Q9fll1 thermosynech	181	6	4.4	231	11	Q9CS11	Q9cs11 mus musculu
109	6	4.4	119	2	Q9KZK3	Q9kzK3 streptomyc	182	6	4.4	232	5	Q17525	Q17525 caenorhabdi
110	6	4.4	123	10	Q9XPM3	Q9xfm3 dianthus ca	183	6	4.4	234	2	Q06424	Q06424 mycobacteri
111	6	4.4	129	8	Q9BBH0	Q9bbh0 swertia voi	184	6	4.4	237	10	Q9FHR2	Q9fhr2 arabisdopsis
112	6	4.4	135	11	Q9CQN7	Q9cqn7 mus musculu	185	6	4.4	241	2	P94514	P94514 bacillus su
113	6	4.4	138	2	Q9WXS5	Q9wxs5 thermotoga	186	6	4.4	241	2	Q9ACH4	Q9ach4 uncultured
114	6	4.4	141	2	Q9JS86	Q9js86 chlamydia p	187	6	4.4	241	2	Q9ACH3	Q9ach3 uncultured
115	6	4.4	144	11	Q9RIG0	Q9rig0 rattus norv	188	6	4.4	241	2	Q9ACH2	Q9ach2 uncultured
116	6	4.4	146	5	Q45175	Q45175 caenorhabdi	189	6	4.4	241	2	Q9ACH1	Q9ach1 uncultured
117	6	4.4	158	2	Q9KCB0	Q9kcb0 bacillus na	190	6	4.4	241	2	Q9ACH0	Q9ach0 uncultured
118	6	4.4	159	5	Q9VAK5	Q9vak5 drosophila	191	6	4.4	242	2	Q53416	Q53416 bradyrhizob
119	6	4.4	162	2	Q9C140	Q9c140 lactococcus	192	6	4.4	243	2	P77222	P77222 escherichia
120	6	4.4	162	9	Q9AZD6	Q9azd6 bacterioph	193	6	4.4	244	10	Q9M1W8	Q9m1w8 arabisdopsis
121	6	4.4	164	10	Q9C910	Q9c910 arabisdopsis	194	6	4.4	247	4	Q9NXZ6	Q9nxz6 homo sapien
122	6	4.4	165	10	Q65155	Q65155 arabisdopsis	195	6	4.4	248	2	P76119	P76119 escherichia
123	6	4.4	166	2	Q66981	Q66981 aquifex ae	196	6	4.4	250	5	Q9VBV1	Q9vbv1 drosophila
124	6	4.4	166	10	Q9XEB2	Q9xeb2 arabisdopsis	197	6	4.4	250	8	Q9G916	Q9g916 ochromonas
125	6	4.4	169	12	Q9QFZ2	Q9qfz2 human immun	198	6	4.4	252	2	Q9RMK7	Q9rmk7 delinococcus
126	6	4.4	171	11	Q9CYX8	Q9cyx8 mus musculu	199	6	4.4	253	2	P96151	P96151 vibrio chol
127	6	4.4	173	5	Q01354	Q01354 halocynthia	200	6	4.4	254	2	Q9KOF0	Q9kof0 vibrio chol
128	6	4.4	175	2	Q910A9	Q910a9 pseudomonas	201	6	4.4	260	13	Q9PU19	Q9pu19 xenopus lae
129	6	4.4	177	10	Q9L178	Q9l178 arabisdopsis	202	6	4.4	265	3	Q12044	Q12044 saccharomyc
130	6	4.4	179	2	Q9XCNO	Q9xcn0 helicobacte	203	6	4.4	269	10	Q9S972	Q9s972 arabisdopsis
131	6	4.4	180	10	Q8SSY1	Q8ssy1 cucumis sat	204	6	4.4	270	2	Q9XAK5	Q9xak5 streptomyc
132	6	4.4	183	9	Q9G0Z7	Q9g0z7 bacterioph	205	6	4.4	272	2	Q9A0N8	Q9a0n8 streptococ
133	6	4.4	186	9	Q9T169	Q9t169 bacterioph	206	6	4.4	272	5	P90762	P90762 caenorhabdi
134	6	4.4	187	2	Q9EE00	Q9ee00 human immun	207	6	4.4	272	12	Q9EHA6	Q9eha6 human immun
135	6	4.4	187	2	Q50716	Q50716 borrelia bu	208	6	4.4	273	4	Q9HD12	Q9hd12 homo sapien
136	6	4.4	191	10	Q9ZUF7	Q9zuf7 arabisdopsis	209	6	4.4	273	12	Q9J5E1	Q9j5e1 fowlpox vir
137	6	4.4	192	10	Q9S7F8	Q9syf7 arabisdopsis	210	6	4.4	274	10	Q9T083	Q9t083 arabisdopsis
138	6	4.4	193	4	Q14426	Q14426 homo sapien	211	6	4.4	275	2	Q50711	Q50711 mycobacteri
139	6	4.4	194	10	Q9SY68	Q9sy68 arabisdopsis	212	6	4.4	275	2	Q9RBF3	Q9rbf3 alcaligenes
140	6	4.4	195	2	Q9WXG4	Q9wxg4 rhodococcus	213	6	4.4	275	2	Q9Z821	Q9z821 chlamydia p
141	6	4.4	199	2	Q9PM27	Q9pm27 campylobact	214	6	4.4	275	11	Q9JLE2	Q9jle2 bacillus ha
142	6	4.4	200	2	Q9CJ42	Q9cj42 lactococcus	215	6	4.4	275	11	Q9JLE2	Q9jle2 mus musculu
143	6	4.4	200	4	Q14426	Q14426 homo sapien	216	6	4.4	276	4	Q9NT55	Q9nt55 mus musculu
144	6	4.4	201	1	Q9HSE2	Q9hse2 halobacteri	217	6	4.4	277	2	Q9ZK43	Q9zk43 helicobacte
145	6	4.4	204	5	Q9NS28	Q9ns28 caenorhabdi	218	6	4.4	278	5	Q01411	Q01411 teladorsagi
146	6	4.4	205	12	Q88288	Q88288 snakehead r	219	6	4.4	278	5	Q76646	Q76646 haemonchus
147	6	4.4	209	12	Q9IMT6	Q9im65 lassa virus	220	6	4.4	278	5	Q01410	Q01410 teladorsagi
148	6	4.4	209	12	Q9IMT5	Q9im55 lassa virus	221	6	4.4	278	5	Q9CNP7	Q9cnp7 caenorhabdi
149	6	4.4	209	12	Q9IMT4	Q9im45 lassa virus	222	6	4.4	279	2	Q9ZB12	Q9zb12 leucostoc
150	6	4.4	209	12	Q9IMT2	Q9im12 lassa virus	223	6	4.4	279	2	P96923	P96923 mycobacteri
151	6	4.4	209	12	Q9IMT1	Q9im11 lassa virus	224	6	4.4	279	2	Q9P0U8	Q9pu8 ureaplasma
152	6	4.4	210	2	Q06405	Q06405 mycobacteri	225	6	4.4	279	4	Q9BTU2	Q9btu2 homo sapien
153	6	4.4	210	12	Q9IMT3	Q9im13 lassa virus	226	6	4.4	279	12	Q9WBS3	Q9wbs3 physalis se
154	6	4.4	210	12	Q9IMT0	Q9im10 lassa virus	227	6	4.4	279	12	Q9JH60	Q9jh60 melon yello
155	6	4.4	210	12	Q9IMH9	Q9imh9 lassa virus	228	6	4.4	280	5	Q25597	Q25597 onchocerca
156	6	4.4	210	12	Q9IMH2	Q9imh2 lassa virus	229	6	4.4	280	5	Q9NGY0	Q9ngy0 druglia mala
157	6	4.4	210	12	Q9IMH4	Q9imh4 lassa virus	230	6	4.4	281	5	Q9NGY1	Q9ngy1 drifilaria
158	6	4.4	211	2	Q9EYL7	Q9eyl7 listeria mo	231	6	4.4	282	5	Q16558	Q16558 caenorhabdi
159	6	4.4	211	2	Q9AK92	Q9ak92 streptomyc	232	6	4.4	286	12	Q9JGU0	Q9jgu0 northern ce
160	6	4.4	211	11	Q55027	Q55027 mus musculu	233	6	4.4	290	2	Q87563	Q87563 bacillus fi
161	6	4.4	215	5	Q21354	Q21354 caenorhabdi	234	6	4.4	292	2	Q25452	Q25452 helicobacte
162	6	4.4	215	5	Q21354	Q21354 caenorhabdi	235	6	4.4	292	2	Q9ZL86	Q9zL86 helicobacte
163	6	4.4	216	5	Q9UF61	Q9uf61 homo sapien	236	6	4.4	292	4	Q9H0V8	Q9h0v8 homo sapien
164	6	4.4	216	5	Q17526	Q17526 caenorhabdi	237	6	4.4	295	2	Q69877	Q69877 streptomyc
165	6	4.4	218	2	Q32851	Q32851 mycobacteri	238	6	4.4	295	5	Q9VIX0	Q9vix0 drosophila

239	6	4.4	297	1	026503	026503 methanobact	312	6	4.4	344	12	09QM05	09qmu5 influenza b
240	6	4.4	299	2	09ZMX9	09zmx9 helicobacte	313	6	4.4	344	12	09QM02	09qmu2 influenza b
241	6	4.4	299	2	09X440	09x440 helicobacte	314	6	4.4	345	12	082638	082638 influenza b
242	6	4.4	299	2	09X439	09x439 helicobacte	315	6	4.4	345	12	082640	082640 influenza b
243	6	4.4	299	2	09X435	09x435 helicobacte	316	6	4.4	345	12	082641	082641 influenza b
244	6	4.4	300	2	09KGN3	09kgn3 bacillus ha	317	6	4.4	345	12	082642	082642 influenza b
245	6	4.4	301	2	09KZP5	09kzp5 streptomyce	318	6	4.4	345	12	082643	082643 influenza b
246	6	4.4	301	2	052494	052494 burkholderi	319	6	4.4	345	12	082645	082645 influenza b
247	6	4.4	302	2	09K7X6	09k7x6 bacillus ha	320	6	4.4	345	12	082647	082647 influenza b
248	6	4.4	304	5	045705	045705 caenorhabdi	321	6	4.4	345	12	082648	082648 influenza b
249	6	4.4	307	5	09NMD3	09nmd3 drosophila	322	6	4.4	345	12	082652	082652 influenza b
250	6	4.4	308	5	09VHC8	09vhc8 drosophila	323	6	4.4	345	12	082653	082653 influenza b
251	6	4.4	315	2	09Z489	09z489 listeria iv	324	6	4.4	345	12	082639	082639 influenza b
252	6	4.4	315	12	09Q0B8	09q0b8 yaba monkey	325	6	4.4	345	12	082655	082655 influenza b
253	6	4.4	316	2	09KTJ3	09ktj3 vibrio chol	326	6	4.4	345	12	082655	082655 influenza b
254	6	4.4	316	12	09J587	09j587 fowlpox vir	327	6	4.4	345	12	09YWM7	09ywj7 influenza b
255	6	4.4	316	12	09DH01	09dh01 yaba-like d	328	6	4.4	345	12	09YWM7	09ywj7 influenza b
256	6	4.4	321	2	09KCO2	09kcg2 bacillus ha	329	6	4.4	345	12	09YWM6	09ywj6 influenza b
257	6	4.4	322	2	09KCB6	09kcb6 bacillus ha	330	6	4.4	345	12	09YWM5	09ywj5 influenza b
258	6	4.4	323	2	09AKG4	09akg4 rickettsia	331	6	4.4	345	12	09YWM4	09ywj4 influenza b
259	6	4.4	323	5	044200	044200 bombyx mori	332	6	4.4	345	12	09YWM2	09ywj2 influenza b
260	6	4.4	324	5	001479	001479 caenorhabdi	333	6	4.4	345	12	09YWM2	09ywj2 influenza b
261	6	4.4	326	2	09ZEX9	09zex9 helicobacte	334	6	4.4	345	12	09YWM1	09ywj1 influenza b
262	6	4.4	328	12	096697	096697 canine herp	335	6	4.4	345	12	09YWM0	09ywj0 influenza b
263	6	4.4	328	12	09QEM3	09qem3 human immun	336	6	4.4	345	12	09YMT9	09ymj9 influenza b
264	6	4.4	328	12	09EKD3	09ekd3 human immun	337	6	4.4	345	12	09YMT8	09ymj8 influenza b
265	6	4.4	328	12	09EKD3	09ekd3 human immun	338	6	4.4	345	12	09YMT7	09ymj7 influenza b
266	6	4.4	328	12	09EKD3	09ekd3 human immun	339	6	4.4	345	12	09YMT6	09ymj6 influenza b
267	6	4.4	328	12	09EJ44	09ej44 human immun	340	6	4.4	345	12	09YMT5	09ymj5 influenza b
268	6	4.4	328	12	09EJ21	09ej21 human immun	341	6	4.4	345	12	09YMT4	09ymj4 influenza b
269	6	4.4	328	12	09ETB3	09etb3 human immun	342	6	4.4	345	12	09YMT3	09ymj3 influenza b
270	6	4.4	328	12	09ETB1	09etb1 human immun	343	6	4.4	345	12	09YMT2	09ymj2 influenza b
271	6	4.4	328	12	09EH99	09eh99 human immun	344	6	4.4	345	12	09YMT1	09ymj1 influenza b
272	6	4.4	328	12	09EH92	09eh92 human immun	345	6	4.4	345	12	09YMT0	09ymj0 influenza b
273	6	4.4	328	12	09EH88	09eh88 human immun	346	6	4.4	345	12	09YMN9	09ymj9 influenza b
274	6	4.4	328	12	09EH87	09eh87 human immun	347	6	4.4	345	12	09YMN8	09ymj8 influenza b
275	6	4.4	328	12	09EH77	09eh77 human immun	348	6	4.4	345	12	09YMN7	09ymj7 influenza b
276	6	4.4	328	12	09EH75	09eh75 human immun	349	6	4.4	345	12	09YMN6	09ymj6 influenza b
277	6	4.4	328	12	09EH69	09eh69 human immun	350	6	4.4	345	12	09YMN5	09ymj5 influenza b
278	6	4.4	328	12	09EH68	09eh68 human immun	351	6	4.4	345	12	09YMN4	09ymj4 influenza b
279	6	4.4	328	12	09EH66	09eh66 human immun	352	6	4.4	345	12	09YMN3	09ymj3 influenza b
280	6	4.4	328	12	09EH65	09eh65 human immun	353	6	4.4	345	12	09YMN2	09ymj2 influenza b
281	6	4.4	328	12	09EH63	09eh63 human immun	354	6	4.4	345	12	09YMN1	09ymj1 influenza b
282	6	4.4	328	12	09EH62	09eh62 human immun	355	6	4.4	345	12	09YMN0	09ymj0 influenza b
283	6	4.4	328	12	09EH61	09eh61 human immun	356	6	4.4	345	12	09YMG9	09ymj9 influenza b
284	6	4.4	328	12	09EH60	09eh60 human immun	357	6	4.4	345	12	09YMG8	09ymj8 influenza b
285	6	4.4	328	12	09EH57	09eh57 human immun	358	6	4.4	345	12	09YML8	09yml8 influenza b
286	6	4.4	328	12	09EH56	09eh56 human immun	359	6	4.4	345	12	09YMD3	09ymd3 influenza b
287	6	4.4	328	12	09EH50	09eh50 human immun	360	6	4.4	345	12	09YMD2	09ymd2 influenza b
288	6	4.4	328	12	09EH47	09eh47 human immun	361	6	4.4	345	12	09YMD9	09ymd9 influenza b
289	6	4.4	328	12	09ED27	09ed27 human immun	362	6	4.4	345	12	09QMU1	09qmu1 influenza b
290	6	4.4	328	12	09ED23	09ed23 human immun	363	6	4.4	345	12	09QMU0	09qmu0 influenza b
291	6	4.4	328	12	09EDW8	09edw8 human immun	364	6	4.4	345	12	09QMT7	09qmt7 influenza b
292	6	4.4	328	12	09EDW5	09edw5 human immun	365	6	4.4	345	12	09QMS4	09qms4 influenza b
293	6	4.4	328	12	09EDK1	09edk1 human immun	366	6	4.4	346	12	09YMG7	09ymg7 influenza b
294	6	4.4	328	12	09EDG0	09edg0 human immun	367	6	4.4	346	12	09YMG6	09ymg6 influenza b
295	6	4.4	328	12	09EDAO	09eda0 human immun	368	6	4.4	346	12	09YMG5	09ymg5 influenza b
296	6	4.4	328	12	09EDC3	09ecc3 human immun	369	6	4.4	346	12	09YMG4	09ymg4 influenza b
297	6	4.4	331	5	020774	020774 caenorhabdi	370	6	4.4	346	12	09YMG3	09ymg3 influenza b
298	6	4.4	331	12	09OAV7	09oav7 influenza b	371	6	4.4	346	12	09YMG2	09ymg2 influenza b
299	6	4.4	332	5	044895	044895 caenorhabdi	372	6	4.4	346	12	09YMG1	09ymg1 influenza b
300	6	4.4	332	2	053339	053339 rhizobium m	373	6	4.4	346	12	09YMG0	09ymg0 influenza b
301	6	4.4	334	10	09LW3	09lww3 arabidopsis	374	6	4.4	346	12	09YMF9	09ymf9 influenza b
302	6	4.4	335	12	09OAV6	09oav6 influenza b	375	6	4.4	346	12	09YMF8	09ymf8 influenza b
303	6	4.4	335	12	09OAV5	09oav5 influenza b	376	6	4.4	346	12	09YMF7	09ymf7 influenza b
304	6	4.4	336	12	09WPR9	09wpr9 influenza b	377	6	4.4	346	12	09YMF6	09ymf6 influenza b
305	6	4.4	337	5	09VHN7	09vhn7 drosophila	378	6	4.4	346	12	09YMF5	09ymf5 influenza b
306	6	4.4	338	2	09AJU0	09aju0 kurtshia sp.	379	6	4.4	346	12	09YMF4	09ymf4 influenza b
307	6	4.4	340	12	098YT4	098yt4 human immun	380	6	4.4	346	12	09YMF3	09ymf3 influenza b
308	6	4.4	341	12	09BWR1	09bwr1 human immun	381	6	4.4	346	12	09YMF2	09ymf2 influenza b
309	6	4.4	343	2	09RVS6	09rvs6 delinococcus	382	6	4.4	346	12	09YMF1	09ymf1 influenza b
310	6	4.4	344	12	09WDB1	09wdb1 influenza b	383	6	4.4	346	12	09YWF0	09ywf0 influenza b
311	6	4.4	344	12	09WDB0	09wdb0 influenza b	384	6	4.4	346	12	09YWF9	09ywf9 influenza b

385	6	4.4	346	12	Q9YWE8	Q9YWE8 Influenza b	458	6	4.4	348	12	Q9OAV4	Q9gav4 Influenza b
386	6	4.4	346	12	Q9YWE7	Q9YWE7 Influenza b	459	6	4.4	348	12	Q9OAV3	Q9gav3 Influenza b
387	6	4.4	346	12	Q9YWE6	Q9YWE6 Influenza b	460	6	4.4	348	12	Q9YI65	Q9y165 Influenza b
388	6	4.4	346	12	Q9YWE5	Q9YWE5 Influenza b	461	6	4.4	349	12	067095	067095 aquifex aeo
389	6	4.4	346	12	Q9YWE4	Q9YWE4 Influenza b	462	6	4.4	349	12	Q9WSR7	Q9wsr7 Influenza b
390	6	4.4	346	12	Q9YWE3	Q9YWE3 Influenza b	463	6	4.4	349	12	Q9YI66	Q9y166 Influenza b
391	6	4.4	346	12	Q9YWE2	Q9YWE2 Influenza b	464	6	4.4	350	2	Q9RZ91	Q9rzt91 delinococcus
392	6	4.4	346	12	Q9YWE1	Q9YWE1 Influenza b	465	6	4.4	350	2	Q9EVJ8	Q9evj8 corynebacte
393	6	4.4	346	12	Q9YWE0	Q9YWE0 Influenza b	466	6	4.4	350	12	Q9WSR3	Q9wsr3 Influenza b
394	6	4.4	346	12	Q9YWD9	Q9YWD9 Influenza b	467	6	4.4	351	4	Q9NUT8	Q9nut8 homo sapien
395	6	4.4	346	12	Q9YWD8	Q9YWD8 Influenza b	468	6	4.4	351	4	Q9BV76	Q9bv76 homo sapien
396	6	4.4	346	12	Q9YWD7	Q9YWD7 Influenza b	469	6	4.4	351	12	Q9WSS1	Q9wss1 Influenza b
397	6	4.4	346	12	Q9YWD6	Q9YWD6 Influenza b	470	6	4.4	351	12	Q9YI61	Q9y161 Influenza b
398	6	4.4	346	12	Q9YWD5	Q9YWD5 Influenza b	471	6	4.4	352	4	Q9BTR6	Q9btr6 homo sapien
399	6	4.4	346	12	Q9YWD4	Q9YWD4 Influenza b	472	6	4.4	352	12	Q9OKD9	Q9okd9 Influenza b
400	6	4.4	346	12	Q9YWD3	Q9YWD3 Influenza b	473	6	4.4	352	12	Q9OKD8	Q9okd8 Influenza b
401	6	4.4	346	12	Q9YWD2	Q9YWD2 Influenza b	474	6	4.4	352	12	Q9OKD7	Q9okd7 Influenza b
402	6	4.4	346	12	Q9YWD1	Q9YWD1 Influenza b	475	6	4.4	352	12	Q9YI62	Q9y162 Influenza b
403	6	4.4	346	12	Q9YWD0	Q9YWD0 Influenza b	476	6	4.4	353	12	Q9WSS2	Q9wss2 Influenza b
404	6	4.4	346	12	Q9YWC9	Q9YWC9 Influenza b	477	6	4.4	353	12	Q9WSR8	Q9wsr8 Influenza b
405	6	4.4	346	12	Q9YWC8	Q9YWC8 Influenza b	478	6	4.4	353	12	Q9OMH0	Q9omh0 Influenza b
406	6	4.4	346	12	Q9YWC7	Q9YWC7 Influenza b	479	6	4.4	354	12	Q9IPJ4	Q9ipj4 Influenza b
407	6	4.4	346	12	Q9YWC6	Q9YWC6 Influenza b	480	6	4.4	355	12	Q9IPJ2	Q9ipj2 Influenza b
408	6	4.4	346	12	Q9YWC5	Q9YWC5 Influenza b	481	6	4.4	355	12	Q9YI60	Q9y160 Influenza b
409	6	4.4	346	12	Q9YWC4	Q9YWC4 Influenza b	482	6	4.4	355	12	Q9WSR6	Q9wsr6 Influenza b
410	6	4.4	346	12	Q9YWC3	Q9YWC3 Influenza b	483	6	4.4	356	12	Q9WSR4	Q9wsr4 Influenza b
411	6	4.4	346	12	Q9YWC2	Q9YWC2 Influenza b	484	6	4.4	356	12	Q9YI63	Q9y163 Influenza b
412	6	4.4	346	12	Q9YWC1	Q9YWC1 Influenza b	485	6	4.4	357	2	Q9YR85	Q9yr85 streptococc
413	6	4.4	346	12	Q9YUJ2	Q9YUJ2 Influenza b	486	6	4.4	358	12	Q9WSR9	Q9wsr9 Influenza b
414	6	4.4	346	12	Q9YUJ1	Q9YUJ1 Influenza b	487	6	4.4	358	12	Q9WRK3	Q9wrk3 Influenza b
415	6	4.4	346	12	Q9YUJ0	Q9YUJ0 Influenza b	488	6	4.4	359	12	Q9WSR5	Q9wsr5 Influenza b
416	6	4.4	346	12	Q9YUC6	Q9YUC6 Influenza b	489	6	4.4	359	12	Q9WSR5	Q9wsr5 Influenza b
417	6	4.4	346	12	Q9YUJ3	Q9YUJ3 Influenza b	490	6	4.4	360	12	Q9YI62	Q9y162 Influenza b
418	6	4.4	346	12	Q9YUJ4	Q9YUJ4 Influenza b	491	6	4.4	360	12	Q9YI63	Q9y163 Influenza b
419	6	4.4	346	12	Q9YUJ5	Q9YUJ5 Influenza b	492	6	4.4	360	12	Q9YI64	Q9y164 Influenza b
420	6	4.4	346	12	Q9YUJ6	Q9YUJ6 Influenza b	493	6	4.4	360	12	Q9YI65	Q9y165 Influenza b
421	6	4.4	346	12	Q9YUJ7	Q9YUJ7 Influenza b	494	6	4.4	360	12	Q9YI66	Q9y166 Influenza b
422	6	4.4	346	12	Q9YUJ8	Q9YUJ8 Influenza b	495	6	4.4	360	12	Q9YI67	Q9y167 Influenza b
423	6	4.4	346	12	Q9YUJ9	Q9YUJ9 Influenza b	496	6	4.4	360	12	Q9YI68	Q9y168 Influenza b
424	6	4.4	346	12	Q9YUJ0	Q9YUJ0 Influenza b	497	6	4.4	360	12	Q9YI69	Q9y169 Influenza b
425	6	4.4	346	12	Q9YUJ1	Q9YUJ1 Influenza b	498	6	4.4	360	12	Q9YI70	Q9y170 Influenza b
426	6	4.4	346	12	Q9YUJ2	Q9YUJ2 Influenza b	499	6	4.4	360	12	Q9YI71	Q9y171 Influenza b
427	6	4.4	346	12	Q9YUJ3	Q9YUJ3 Influenza b	500	6	4.4	360	12	Q9YI72	Q9y172 Influenza b
428	6	4.4	346	12	Q9YUJ4	Q9YUJ4 Influenza b	501	6	4.4	360	12	Q9YI73	Q9y173 Influenza b
429	6	4.4	346	12	Q9YUJ5	Q9YUJ5 Influenza b	502	6	4.4	360	12	Q9YI74	Q9y174 Influenza b
430	6	4.4	346	12	Q9YUJ6	Q9YUJ6 Influenza b	503	6	4.4	360	12	Q9YI75	Q9y175 Influenza b
431	6	4.4	346	12	Q9YUJ7	Q9YUJ7 Influenza b	504	6	4.4	360	12	Q9YI76	Q9y176 Influenza b
432	6	4.4	346	12	Q9YUJ8	Q9YUJ8 Influenza b	505	6	4.4	360	12	Q9YI77	Q9y177 Influenza b
433	6	4.4	346	12	Q9YUJ9	Q9YUJ9 Influenza b	506	6	4.4	360	12	Q9YI78	Q9y178 Influenza b
434	6	4.4	347	12	Q9YUJ0	Q9YUJ0 Influenza b	507	6	4.4	361	12	Q9YI79	Q9y179 Influenza b
435	6	4.4	347	12	Q9YUJ1	Q9YUJ1 Influenza b	508	6	4.4	361	12	Q9YI80	Q9y180 Influenza b
436	6	4.4	347	12	Q9YUJ2	Q9YUJ2 Influenza b	509	6	4.4	361	12	Q9YI81	Q9y181 Influenza b
437	6	4.4	347	12	Q9YUJ3	Q9YUJ3 Influenza b	510	6	4.4	361	12	Q9YI82	Q9y182 Influenza b
438	6	4.4	347	12	Q9YUJ4	Q9YUJ4 Influenza b	511	6	4.4	361	12	Q9YI83	Q9y183 Influenza b
439	6	4.4	347	12	Q9YUJ5	Q9YUJ5 Influenza b	512	6	4.4	361	12	Q9YI84	Q9y184 Influenza b
440	6	4.4	347	12	Q9YUJ6	Q9YUJ6 Influenza b	513	6	4.4	361	12	Q9YI85	Q9y185 Influenza b
441	6	4.4	347	12	Q9YUJ7	Q9YUJ7 Influenza b	514	6	4.4	361	12	Q9YI86	Q9y186 Influenza b
442	6	4.4	347	12	Q9YUJ8	Q9YUJ8 Influenza b	515	6	4.4	361	12	Q9YI87	Q9y187 Influenza b
443	6	4.4	347	12	Q9YUJ9	Q9YUJ9 Influenza b	516	6	4.4	361	12	Q9YI88	Q9y188 Influenza b
444	6	4.4	347	12	Q9YUJ0	Q9YUJ0 Influenza b	517	6	4.4	361	12	Q9YI89	Q9y189 Influenza b
445	6	4.4	347	12	Q9YUJ1	Q9YUJ1 Influenza b	518	6	4.4	361	12	Q9YI90	Q9y190 Influenza b
446	6	4.4	347	12	Q9YUJ2	Q9YUJ2 Influenza b	519	6	4.4	361	12	Q9YI91	Q9y191 Influenza b
447	6	4.4	347	12	Q9YUJ3	Q9YUJ3 Influenza b	520	6	4.4	361	12	Q9YI92	Q9y192 Influenza b
448	6	4.4	347	12	Q9YUJ4	Q9YUJ4 Influenza b	521	6	4.4	361	12	Q9YI93	Q9y193 Influenza b
449	6	4.4	347	12	Q9YUJ5	Q9YUJ5 Influenza b	522	6	4.4	361	12	Q9YI94	Q9y194 Influenza b
450	6	4.4	347	12	Q9YUJ6	Q9YUJ6 Influenza b	523	6	4.4	361	12	Q9YI95	Q9y195 Influenza b
451	6	4.4	347	12	Q9YUJ7	Q9YUJ7 Influenza b	524	6	4.4	361	12	Q9YI96	Q9y196 Influenza b
452	6	4.4	347	12	Q9YUJ8	Q9YUJ8 Influenza b	525	6	4.4	361	12	Q9YI97	Q9y197 Influenza b
453	6	4.4	347	12	Q9YUJ9	Q9YUJ9 Influenza b	526	6	4.4	361	12	Q9YI98	Q9y198 Influenza b
454	6	4.4	347	12	Q9YUJ0	Q9YUJ0 Influenza b	527	6	4.4	361	12	Q9YI99	Q9y199 Influenza b
455	6	4.4	347	12	Q9YUJ1	Q9YUJ1 Influenza b	528	6	4.4	361	12	Q9YI00	Q9y200 Influenza b
456	6	4.4	347	12	Q9YUJ2	Q9YUJ2 Influenza b	529	6	4.4	361	12	Q9YI01	Q9y201 Influenza b
457	6	4.4	348	2	Q9I4X1	Q9I4X1 pseudomonas	530	6	4.4	362	12	Q9YI02	Q9y202 Influenza b

531	6	4.4	363	12	091UY5	Q91Y5 influenza b	604	6	4.4	421	1	09Y800	Q9Y80 aeropyrum p
532	6	4.4	363	12	091UY3	Q91Y3 influenza b	605	6	4.4	424	2	091232	Q91232 pseudomonas
533	6	4.4	363	12	091UY2	Q91Y2 influenza b	606	6	4.4	424	5	016594	Q16594 caenorhabdi
534	6	4.4	363	12	091UY1	Q91Y1 influenza b	607	6	4.4	424	10	09SVK8	Q9SVK8 aradidopsi
535	6	4.4	364	3	Q9P8N0	Q9P8N0 pichia angu	608	6	4.4	425	1	059010	059010 pyrococcus
536	6	4.4	364	12	084081	084081 influenza b	609	6	4.4	425	1	09V0E7	Q9V0E7 pyrococcus
537	6	4.4	365	4	Q9H909	Q9H909 homo sapien	610	6	4.4	426	1	09H06	Q9H06 halobacteri
538	6	4.4	365	10	Q9R035	Q9R035 aradidopsi	611	6	4.4	426	10	Q9S0L7	Q9S0L7 aradidopsi
539	6	4.4	366	12	Q9AVR1	Q9AVR1 stephanotis	612	6	4.4	429	5	044842	044842 caenorhabdi
540	6	4.4	366	12	084076	084076 influenza b	613	6	4.4	431	2	Q9KLR1	Q9KLR1 vibrio chol
541	6	4.4	367	1	Q9HRA3	Q9HRA3 halobacteri	614	6	4.4	433	1	028602	028602 archaeoglob
542	6	4.4	368	12	Q9WPS3	Q9WPS3 influenza b	615	6	4.4	433	5	09V438	Q9V438 drosophila
543	6	4.4	369	10	Q9LKH6	Q9LKH6 aradidopsi	616	6	4.4	433	5	Q9NK40	Q9NK40 drosophila
544	6	4.4	371	5	Q9N470	Q9N470 caenorhabdi	617	6	4.4	434	5	Q9VAT9	Q9VAT9 drosophila
545	6	4.4	371	12	Q98220	Q98220 human immun	618	6	4.4	435	2	09K832	Q9K832 bacillus ha
546	6	4.4	373	2	051151	051151 neisseria m	619	6	4.4	435	10	09PPA2	09PPA2 oryza sativ
547	6	4.4	373	6	097932	097932 ovis aries	620	6	4.4	436	2	051415	051415 boerelia bu
548	6	4.4	373	10	09ZYC1	Q9ZYC1 aradidopsi	621	6	4.4	436	5	09XTU8	Q9XTU8 caenorhabdi
549	6	4.4	374	10	09FRC8	Q9FRC8 aradidopsi	622	6	4.4	438	2	Q9CBK3	Q9CBK3 mycobacteri
550	6	4.4	376	2	052711	052711 saccharopol	623	6	4.4	438	5	Q20252	Q20252 caenorhabdi
551	6	4.4	376	6	046499	046499 bos taurus	624	6	4.4	438	5	09VJQ3	Q9VJQ3 drosophila
552	6	4.4	376	6	Q9TXX4	Q9TXX4 capra hircu	625	6	4.4	440	2	0919C1	Q919C1 azoarcus ev
553	6	4.4	376	10	049315	049315 aradidopsi	626	6	4.4	440	5	077369	077369 plasmodium
554	6	4.4	376	10	Q9SMS5	Q9SMS5 aradidopsi	627	6	4.4	441	2	09RUT7	Q9RUT7 streptomyc
555	6	4.4	377	2	Q9XSE8	Q9XSE8 streptomyc	628	6	4.4	443	2	Q9LIB6	Q9LIB6 pseudomonas
556	6	4.4	377	3	074794	074794 schistosach	629	6	4.4	447	2	Q9RUD3	Q9RUD3 deinococcus
557	6	4.4	377	5	Q9U053	Q9U053 giardia lam	630	6	4.4	450	2	Q9KEX2	Q9KEX2 bacillus ha
558	6	4.4	377	5	Q9XVP3	Q9XVP3 caenorhabdi	631	6	4.4	452	11	Q9CXM9	Q9CXM9 mus musculu
559	6	4.4	377	12	Q9WPS2	Q9WPS2 influenza b	632	6	4.4	453	2	Q9KNH7	Q9KNH7 mus musculu
560	6	4.4	378	12	084102	084102 influenza b	633	6	4.4	455	2	053182	053182 rhodobacter
561	6	4.4	378	12	067362	067362 influenza b	634	6	4.4	455	2	Q9S228	Q9S228 rhodobacter
562	6	4.4	378	12	067364	067364 influenza b	635	6	4.4	458	12	Q9WPS1	Q9WPS1 influenza b
563	6	4.4	378	12	067365	067365 influenza b	636	6	4.4	459	11	Q9JLM3	Q9JLM3 mus musculu
564	6	4.4	378	12	067367	067367 influenza b	637	6	4.4	461	11	Q9DCV1	Q9DCV1 mus musculu
565	6	4.4	378	12	067368	067368 influenza b	638	6	4.4	463	10	Q39871	Q39871 glycine max
566	6	4.4	379	5	Q9UIC2	Q9UIC2 leishmania	639	6	4.4	464	5	015827	015827 leishmania
567	6	4.4	379	5	Q9BLM4	Q9BLM4 leishmania	640	6	4.4	465	2	082877	082877 streptococ
568	6	4.4	379	12	067363	067363 influenza b	641	6	4.4	465	10	Q43166	Q43166 solanum tub
569	6	4.4	379	12	067366	067366 influenza b	642	6	4.4	466	5	Q93712	Q93712 caenorhabdi
570	6	4.4	380	12	Q9LIX8	Q9LIX8 influenza b	643	6	4.4	466	10	Q43526	Q43526 lycopersico
571	6	4.4	383	2	Q9RS15	Q9RS15 deinococcus	644	6	4.4	467	1	Q93661	Q93661 methanosarc
572	6	4.4	389	2	Q9RUT7	Q9RUT7 streptomyc	645	6	4.4	467	10	081143	081143 lycopersico
573	6	4.4	391	5	Q9BUT6	Q9BUT6 tetrahymena	646	6	4.4	468	4	Q9Y4B8	Q9Y4B8 homo sapien
574	6	4.4	392	4	Q9B0U6	Q9B0U6 homo sapien	647	6	4.4	468	10	081722	081722 aradidopsi
575	6	4.4	394	10	Q9FJZ1	Q9FJZ1 aradidopsi	648	6	4.4	470	11	Q62965	Q62965 rattus norv
576	6	4.4	394	12	Q9WPS4	Q9WPS4 influenza b	649	6	4.4	471	5	Q9VES7	Q9VES7 drosophila
577	6	4.4	394	12	Q9QTH9	Q9QTH9 svts2 plect	650	6	4.4	471	5	Q9VES6	Q9VES6 drosophila
578	6	4.4	396	1	Q9HS71	Q9HS71 halobacteri	651	6	4.4	474	5	Q9BKJ3	Q9BKJ3 giardia lam
579	6	4.4	397	6	Q28546	Q28546 ovis aries	652	6	4.4	476	2	Q9KLD4	Q9KLD4 vibrio chol
580	6	4.4	397	11	Q9EBJ1	Q9EBJ1 rattus norv	653	6	4.4	476	10	P93365	P93365 nicotiana t
581	6	4.4	397	11	Q9CWK7	Q9CWK7 mus musculu	654	6	4.4	476	10	Q9AT54	Q9AT54 nicotiana t
582	6	4.4	398	4	Q9UE68	Q9UE68 homo sapien	655	6	4.4	480	4	Q9HLP3	Q9HLP3 homo sapien
583	6	4.4	398	5	Q18884	Q18884 caenorhabdi	656	6	4.4	480	5	Q9BHJ7	Q9BHJ7 trypanosoma
584	6	4.4	399	4	Q9H7J3	Q9H7J3 homo sapien	657	6	4.4	481	5	Q22539	Q22539 caenorhabdi
585	6	4.4	402	2	Q99VB0	Q99VB0 streptococ	658	6	4.4	482	10	082443	082443 zea mays (m
586	6	4.4	402	10	Q9LJZ8	Q9LJZ8 aradidopsi	659	6	4.4	483	2	Q56622	Q56622 vibrio chol
587	6	4.4	406	10	Q9FE30	Q9FE30 aradidopsi	660	6	4.4	483	10	087164	087164 oryza sativ
588	6	4.4	407	2	067720	067720 aquifex aeo	661	6	4.4	483	10	09S768	Q9S768 oryza sativ
589	6	4.4	407	10	Q9ZOA3	Q9ZOA3 aradidopsi	662	6	4.4	486	2	Q9L378	Q9L378 bacillus sp
590	6	4.4	408	4	Q16670	Q16670 homo sapien	663	6	4.4	486	2	Q9KW38	Q9KW38 wolbachia s
591	6	4.4	409	1	Q9YAC7	Q9YAC7 aeropyrum p	664	6	4.4	486	10	Q9M1W0	Q9M1W0 aradidopsi
592	6	4.4	410	2	Q9L446	Q9L446 streptococ	665	6	4.4	489	2	P71048	P71048 bacillus su
593	6	4.4	410	2	Q9L445	Q9L445 streptococ	666	6	4.4	493	5	Q23330	Q23330 caenorhabdi
594	6	4.4	410	2	Q9L444	Q9L444 streptococ	667	6	4.4	495	10	Q23330	Q23330 aradidopsi
595	6	4.4	410	2	Q9L388	Q9L388 streptococ	668	6	4.4	496	5	Q18683	Q18683 drosophila
596	6	4.4	410	2	Q9E258	Q9E258 corynebacte	669	6	4.4	503	2	Q9K445	Q9K445 wolbachia s
597	6	4.4	410	2	Q9ANW7	Q9ANW7 streptococ	670	6	4.4	506	10	Q38860	Q38860 aradidopsi
598	6	4.4	412	2	Q25885	Q25885 helicobacte	671	6	4.4	507	11	Q9C739	Q9C739 mus musculu
599	6	4.4	413	5	Q44190	Q44190 caenorhabdi	672	6	4.4	508	5	Q45345	Q45345 caenorhabdi
600	6	4.4	413	1	Q26879	Q26879 methanobact	673	6	4.4	508	5	Q96146	Q96146 plasmodium
601	6	4.4	414	2	Q53279	Q53279 mycobacteri	674	6	4.4	509	5	Q9VTZ7	Q9VTZ7 drosophila
602	6	4.4	416	2	Q45154	Q45154 bacteroides	675	6	4.4	509	10	P93058	P93058 brassica ju
603	6	4.4	418	10	Q9C7U5	Q9C7U5 aradidopsi	676	6	4.4	511	10	Q9LFL2	Q9LFL2 aradidopsi

677	6	4.4	513	10	Q9SD51	Q9sd51 arabidopsis	750	6	4.4	652	10	Q9ZV78	Q9Zv78 arabidopsis
678	6	4.4	513	10	P98188	P98188 vicia sativ	751	6	4.4	662	5	Q9VRV6	Q9vrV6 dirosophila
679	6	4.4	515	2	Q9RLV2	Q9rlv2 lactococcus	752	6	4.4	665	5	Q24966	Q24966 giardia lam
680	6	4.4	518	10	Q9SD15	Q9sd15 arabidopsis	753	6	4.4	672	5	Q44189	Q44189 caenorhabd
681	6	4.4	518	11	Q9RQJ2	Q9eqj2 rattus norv	754	6	4.4	676	2	Q9PEP2	Q9pep2 campylobact
682	6	4.4	522	10	Q9FXB5	Q9fxb5 arabidopsis	755	6	4.4	677	2	Q34323	Q34323 bacillus su
683	6	4.4	523	2	Q91729	Q91729 pseudomonas	756	6	4.4	677	4	Q9HAR0	Q9har0 homo sapien
684	6	4.4	526	10	Q9LZ26	Q9lzz26 arabidopsis	757	6	4.4	678	2	Q54679	Q54679 homo sapien
685	6	4.4	528	3	Q9Y7C8	Q9y7c8 aspergillus	758	6	4.4	684	10	Q9XH27	Q9xh27 streptomyce
686	6	4.4	529	3	Q9HDX7	Q9hdx7 schizosacch	759	6	4.4	686	5	Q96245	Q96245 plasmodium
687	6	4.4	531	5	Q9W2A9	Q9w2a9 dirosophila	760	6	4.4	691	5	Q9NKR7	Q9nkr7 leishmania
688	6	4.4	531	10	Q42582	Q42582 arabidopsis	761	6	4.4	692	2	Q9F2J1	Q9f2j1 streptomyce
689	6	4.4	531	10	Q3STZ3	Q3stz3 arabidopsis	762	6	4.4	694	2	Q9L5M3	Q9l5m3 salmonella
690	6	4.4	532	2	Q9LCB8	Q9lcb8 streptococc	763	6	4.4	700	4	Q9UPF8	Q9upf8 homo sapien
691	6	4.4	532	10	Q9T069	Q9t069 arabidopsis	764	6	4.4	704	5	Q02059	Q02059 caenorhabd
692	6	4.4	533	2	Q99U92	Q99u92 staphylococ	765	6	4.4	706	4	Q9H7N2	Q9h7n2 homo sapien
693	6	4.4	534	5	Q9U211	Q9u211 caenorhabd	766	6	4.4	706	11	Q9D2M5	Q9d2m5 mus musculu
694	6	4.4	535	10	Q49600	Q49600 arabidopsis	767	6	4.4	716	10	Q9FH85	Q9fh85 arabidopsis
695	6	4.4	536	4	Q9ASV4	Q9asv4 arabidopsis	768	6	4.4	717	4	Q9NX10	Q9nx10 homo sapien
696	6	4.4	536	10	Q9NQ09	Q9nq09 homo sapien	769	6	4.4	720	2	Q9X8G8	Q9x8g8 streptomyce
697	6	4.4	537	10	Q9FZ24	Q9fz24 arabidopsis	770	6	4.4	732	5	Q9VY71	Q9vy71 dirosophila
698	6	4.4	538	2	Q9PNT5	Q9pnt5 campylobact	771	6	4.4	732	10	Q04269	Q04269 chlamydomon
699	6	4.4	540	2	Q31716	Q31716 bacillus su	772	6	4.4	732	5	Q17305	Q17305 caenorhabd
700	6	4.4	542	2	Q50025	Q50025 mycobacteri	773	6	4.4	738	2	Q59490	Q59490 lactobacill
701	6	4.4	542	5	Q9U1H6	Q9u1h6 dirosophila	774	6	4.4	738	13	Q98SV5	Q98sv5 xenopus lae
702	6	4.4	543	5	Q76521	Q76521 plasmodium	775	6	4.4	750	6	Q9GK13	Q9gk13 bos taurus
703	6	4.4	545	5	Q44019	Q44019 plasmodium	776	6	4.4	753	5	Q44861	Q44861 caenorhabd
704	6	4.4	545	11	Q08661	Q08661 rattus norv	777	6	4.4	756	10	Q22863	Q22863 arabidopsis
705	6	4.4	546	5	Q9GUC3	Q9guc3 caenorhabd	778	6	4.4	757	1	Q9HSN5	Q9hns5 halobacteri
706	6	4.4	548	2	Q9RMQ9	Q9rmq9 delnoccocus	779	6	4.4	760	2	Q9RKG0	Q9rxg0 delnoccocus
707	6	4.4	550	2	Q9C1L3	Q9c1l3 lactococcus	780	6	4.4	761	3	Q9HE59	Q9he59 ashbya goss
708	6	4.4	554	12	Q03259	Q03259 chimpanzee	781	6	4.4	764	10	Q9Z067	Q9z067 arabidopsis
709	6	4.4	557	10	Q9FRK3	Q9frk3 arabidopsis	782	6	4.4	765	5	Q26018	Q26018 plasmodium
710	6	4.4	560	12	Q99AV8	Q99av8 human immun	783	6	4.4	767	4	Q75166	Q75166 homo sapien
711	6	4.4	562	12	Q9DM57	Q9dm57 rat cytoyme	784	6	4.4	767	5	Q18163	Q18163 caenorhabd
712	6	4.4	563	11	Q9EQJ3	Q9eqj3 rattus norv	785	6	4.4	768	5	Q9RTE3	Q9rte3 delnoccocus
713	6	4.4	565	2	Q9KML1	Q9kml1 vibrio chol	786	6	4.4	771	5	Q22783	Q22783 caenorhabd
714	6	4.4	565	6	Q97582	Q97582 sus scrofa	787	6	4.4	772	2	Q9RYQ0	Q9ryq0 delnoccocus
715	6	4.4	565	10	Q9LRT9	Q9lrt9 arabidopsis	788	6	4.4	772	5	Q60958	Q60958 leishmania
716	6	4.4	567	12	Q9IWE3	Q9iwe3 influenza b	789	6	4.4	781	10	Q9SF87	Q9sf87 arabidopsis
717	6	4.4	568	10	Q9LOA2	Q9lwa2 arabidopsis	790	6	4.4	782	5	Q20373	Q20373 plasmodium
718	6	4.4	569	5	Q20817	Q20817 acetobacter	791	6	4.4	794	2	Q9X212	Q9x212 thernotoga
719	6	4.4	569	12	Q9IMT7	Q9imt7 lassa virus	792	6	4.4	796	10	Q9FT77	Q9ft77 arabidopsis
720	6	4.4	570	12	Q9IM02	Q9imj5 rattus norv	793	6	4.4	800	3	Q59960	Q59960 saccharomyc
721	6	4.4	570	12	Q98103	Q98103 influenza b	794	6	4.4	805	5	Q9NCN5	Q9ncn5 euplotes ae
722	6	4.4	572	11	Q9JMK5	Q9jmk5 rattus norv	795	6	4.4	806	10	Q9FFZ5	Q9ffz5 arabidopsis
723	6	4.4	579	11	Q9EQJ4	Q9eqj4 rattus norv	796	6	4.4	807	5	Q9GZ12	Q9gz12 caenorhabd
724	6	4.4	579	11	Q9EQJ4	Q9eqj4 rattus norv	797	6	4.4	821	3	Q98581	Q98581 caenorhabd
725	6	4.4	580	2	Q9KMA4	Q9kma4 vibrio chol	798	6	4.4	822	1	Q30286	Q30286 archaeoglob
726	6	4.4	581	3	Q14035	Q14035 schizosacch	799	6	4.4	822	5	Q25751	Q25751 plasmodium
727	6	4.4	582	12	Q84097	Q84097 influenza b	800	6	4.4	837	10	Q9LZC7	Q9lzc7 arabidopsis
728	6	4.4	584	12	Q9W9R2	Q9w9r2 influenza b	801	6	4.4	837	10	Q9LZC7	Q9lzc7 arabidopsis
729	6	4.4	588	10	Q9RCF0	Q9rcf0 arabidopsis	802	6	4.4	839	10	Q9W332	Q9w332 arabidopsis
730	6	4.4	589	2	Q9REC7	Q9rec7 clostridium	803	6	4.4	844	5	Q44476	Q44476 caenorhabd
731	6	4.4	589	13	Q98CK1	Q98ck1 carassius a	804	6	4.4	856	10	Q9MB88	Q9mb88 brassica ol
732	6	4.4	591	2	Q9F1T9	Q9f1t9 clostridium	805	6	4.4	860	3	Q945D3	Q945d3 atarchis hyp
733	6	4.4	591	5	Q9GU24	Q9gu24 entamoeba h	806	6	4.4	862	10	Q94543	Q94543 schizosacch
734	6	4.4	597	10	Q9LUV9	Q9luy9 arabidopsis	807	6	4.4	865	2	Q43319	Q43319 aeromonas c
735	6	4.4	598	2	Q51954	Q51954 borrelia he	808	6	4.4	865	5	Q9F908	Q9f9g8 aeromonas h
736	6	4.4	598	2	Q9XDP2	Q9xpd2 enterobacte	809	6	4.4	865	2	Q9V524	Q9v524 dirosophila
737	6	4.4	600	11	Q55185	Q55185 mus musculu	810	6	4.4	865	13	Q98SN6	Q98sn6 galinus gall
738	6	4.4	603	4	Q9HBD7	Q9hbd7 homo sapien	811	6	4.4	865	10	Q24320	Q24320 plasmodium v
739	6	4.4	604	10	Q9LW37	Q9lwb7 arabidopsis	812	6	4.4	870	10	Q9ZUT6	Q9zul6 arabidopsis
740	6	4.4	604	10	Q9FTB8	Q9ftb8 arabidopsis	813	6	4.4	874	2	Q53493	Q53493 mycobacteri
741	6	4.4	610	5	Q96198	Q96198 arabidopsis	814	6	4.4	876	10	Q42846	Q42846 hordeum vul
742	6	4.4	610	10	Q9ERT8	Q9ert8 plasmodium	815	6	4.4	883	10	Q9LRP0	Q9lrp0 arabidopsis
743	6	4.4	612	2	Q99YI8	Q99yi8 streptococc	816	6	4.4	887	5	Q19469	Q19469 caenorhabd
744	6	4.4	614	9	Q37967	Q37967 bacterioph	817	6	4.4	892	2	Q55676	Q55676 synechocyst
745	6	4.4	631	10	Q37967	Q37967 bacterioph	818	6	4.4	896	10	Q9FENL	Q9feni arabidopsis
746	6	4.4	635	2	Q45820	Q45820 clostridium	819	6	4.4	898	11	Q88193	Q88193 mus musculu
747	6	4.4	640	2	Q915U9	Q915u9 pseudomonas	820	6	4.4	901	11	Q88193	Q88193 mus musculu
748	6	4.4	644	2	Q9CGM3	Q9cgw3 lactococcus	821	6	4.4	902	5	Q9VSAS	Q9vsas dirosophila
749	6	4.4	652	5	Q9U0D4	Q9u0d4 plasmodium	822	6	4.4				

823	6	4.4	902	10	082323	082323 arabidopsis	896	6	4.4	1629	10	004698	004698 pisum sativ
824	6	4.4	909	11	088190	088190 mus musculus	897	6	4.4	1638	4	09y6j4	09y6j4 homo sapien
825	6	4.4	910	9	037959	037959 lactococcus	898	6	4.4	1650	5	077328	077328 plasmodium
826	6	4.4	913	11	088195	088195 mus musculus	899	6	4.4	1712	4	09y6j5	09y6j5 homo sapien
827	6	4.4	914	5	09BMN6	09bm6 caenorhabdi	900	6	4.4	1721	5	09UAR3	09uar3 pacifastacu
828	6	4.4	914	11	088192	088192 mus musculu	901	6	4.4	1742	2	055583	055583 synechocyst
829	6	4.4	914	11	088194	088194 mus musculu	902	6	4.4	1754	4	09U1M2	09u1m2 homo sapien
830	6	4.4	916	4	060502	060502 homo sapien	903	6	4.4	1780	5	09VUC2	09vuc2 drosophila
831	6	4.4	925	5	09N8G2	09n8g2 trypanosoma	904	6	4.4	1787	10	09SJP0	09sjp0 arabidopsis
832	6	4.4	936	2	09KJ17	09kj17 trichodesmi	905	6	4.4	1793	8	09BBM6	09bbm6 lotus japon
833	6	4.4	941	4	09P2S6	09p2s6 homo sapien	906	6	4.4	1872	11	P70208	P70208 mus musculu
834	6	4.4	946	11	088690	088690 mus musculu	907	6	4.4	1883	2	09PFR2	09pfr2 ureaplasma
835	6	4.4	947	5	008667	008667 plasmodium	908	6	4.4	1888	11	088466	088466 mus musculu
836	6	4.4	947	11	088689	088689 mus musculu	909	6	4.4	1894	11	P70206	P70206 mus musculu
837	6	4.4	949	4	09Y4G6	09y4g6 homo sapien	910	6	4.4	1905	13	091823	091823 xenopus lae
838	6	4.4	961	10	065230	065230 arabidopsis	911	6	4.4	1948	11	028189	028189 archaeoglob
839	6	4.4	969	5	017795	017795 caenorhabdi	912	6	4.4	1956	11	062968	062968 rattus norv
840	6	4.4	976	2	09EV17	09ev17 actinomyces	913	6	4.4	1957	11	063554	063554 rattus norv
841	6	4.4	984	2	067280	067280 aquilex aeo	914	6	4.4	1958	11	P70276	P70276 mus musculu
842	6	4.4	987	3	09USU1	09usul schizosacch	915	6	4.4	1968	5	020439	020439 caenorhabdi
843	6	4.4	987	10	09LNC5	09lnc5 arabidopsis	916	6	4.4	2070	10	09M9X3	09m9x3 arabidopsis
844	6	4.4	987	10	09LNC5	019989 caenorhabdi	917	6	4.4	2119	5	09VAN5	09van5 drosophila
845	6	4.4	997	5	024418	024418 drosophila	918	6	4.4	2172	10	048534	048534 arabidopsis
846	6	4.4	1000	6	028737	028737 oryctolagus	919	6	4.4	2206	5	096205	096205 plasmodium
847	6	4.4	1025	5	025693	025693 plasmodium	920	6	4.4	2209	5	097324	097324 plasmodium
848	6	4.4	1025	13	09DEU1	09deul brachydanio	921	6	4.4	2232	5	P91365	P91365 caenorhabdi
849	6	4.4	1029	4	09C099	09c0c9 homo sapien	922	6	4.4	2231	5	022847	022847 caenorhabdi
850	6	4.4	1029	10	09C8T4	09c8t4 arabidopsis	923	6	4.4	2340	2	09ZDP1	09zdp1 rickettsia
851	6	4.4	1030	10	09FNG8	09fng8 arabidopsis	924	6	4.4	2485	5	096134	096134 plasmodium
852	6	4.4	1031	2	09MXJ2	09mxj2 psychromona	925	6	4.4	2567	5	09U0T6	09u0t6 plasmodium
853	6	4.4	1036	1	029316	029316 archaeoglob	926	6	4.4	2841	2	09F8J3	09f8j3 streptomyc
854	6	4.4	1047	2	09RB35	09rb35 cytophaga s	927	6	4.4	3112	5	09NKP1	09nkp1 leishmania
855	6	4.4	1057	2	09CKR5	09ckr5 pasteurilla	928	6	4.4	3194	5	09U8G8	09u8g8 manduca sex
856	6	4.4	1081	5	09U631	09u631 drosophila	929	6	4.4	3394	4	09Y6V0	09y6v0 homo sapien
857	6	4.4	1083	5	09VTT0	09vtt0 drosophila	930	6	4.4	3488	5	P91257	P91257 caenorhabdi
858	6	4.4	1088	10	09F1M1	09f1m1 arabidopsis	931	6	4.4	3978	5	097236	097236 plasmodium
859	6	4.4	1096	10	09LVD9	09lvd9 arabidopsis	932	6	4.4	4150	2	09KIT4	09kit4 streptomyc
860	6	4.4	1103	3	09C2J7	09c2j7 neurospora	933	6	4.4	4345	2	09X4W2	09x4w2 vibrio chol
861	6	4.4	1107	5	09GR76	09gr76 leishmania	934	6	4.4	4547	5	09W343	09w343 drosophila
862	6	4.4	1127	12	0993K9	0993k9 caallitrichi	935	6	4.4	4558	2	09KSI2	09ksi2 vibrio chol
863	6	4.4	1140	5	020299	020299 caenorhabdi	936	6	4.4	4589	5	076506	076506 tetrahymena
864	6	4.4	1189	10	09FNU0	09fnu0 arabidopsis	937	6	4.4	4688	2	09P008	09p008 plasmodium
865	6	4.4	1235	1	026597	026597 methanobact	938	6	4.4	4899	5	09VR81	09vr81 ureaplasma
866	6	4.4	1244	4	000562	000562 homo sapien	939	6	4.4	4967	4	09Z736	09z736 homo sapien
867	6	4.4	1262	4	09BX73	09bx73 homo sapien	940	6	4.4	4967	11	09ERN6	09ern6 mus musculu
868	6	4.4	1262	4	020684	020684 caenorhabdi	941	6	4.4	4968	6	029621	029621 oryctolagus
869	6	4.4	1270	5	062462	062462 caenorhabdi	942	6	4.4	4981	5	077372	077372 plasmodium
870	6	4.4	1272	10	09M197	09m197 arabidopsis	943	6	4.4	5458	5	09U459	09u459 plasmodium
871	6	4.4	1274	10	09YOK2	09yok2 arabidopsis	944	6	4.4	6875	6	028733	028733 oryctolagus
872	6	4.4	1276	10	081059	081059 arabidopsis	945	6	4.4	26926	4	010466	010466 homo sapien
873	6	4.4	1284	2	09POA1	09pqo1 ureaplasma	946	6	4.4	26926	7	047029	047029 enterobacte
874	6	4.4	1291	10	09SFE1	09sfe1 arabidopsis	947	6	3.7	20	10	09S8J5	09s8j5 psophocarpu
875	6	4.4	1300	4	013999	013999 homo sapien	948	6	3.7	22	12	084254	084254 bovine papl
876	6	4.4	1320	10	09C536	09c536 arabidopsis	949	6	3.7	24	10	P82139	P82139 splnacia ol
877	6	4.4	1327	11	061595	061595 mus musculu	950	6	3.7	26	4	09P2U0	09p2u0 homo sapien
878	6	4.4	1330	6	09Y961	09y961 vulpes vulp	951	6	3.7	26	5	09NBB1	09nbb1 drosophila
879	6	4.4	1332	10	09SXB2	09sxb2 arabidopsis	952	6	3.7	26	5	09BLZ7	09blz7 mactiocrache
880	6	4.4	1352	10	09M2D1	09m2d1 arabidopsis	953	6	3.7	26	5	09BLZ6	09blz6 adineta vag
881	6	4.4	1352	10	09C739	09c739 arabidopsis	954	6	3.7	26	8	P92646	P92646 lialis jica
882	6	4.4	1354	4	013464	013464 homo sapien	955	6	3.7	26	8	P92772	P92772 xantusia vi
883	6	4.4	1354	6	077819	077819 oryctolagus	956	6	3.7	26	11	09OVG9	09ovg9 rattus sp.
884	6	4.4	1354	11	P70335	P70335 mus musculu	957	6	3.7	28	11	09QXB4	09qxb4 mus musculu
885	6	4.4	1356	4	014707	014707 homo sapien	958	6	3.7	32	2	09KLE0	09kle0 vibrio chol
886	6	4.4	1364	13	090631	090631 gallus gall	959	6	3.7	32	10	09FV05	09fv05 zea mays su
887	6	4.4	1369	5	017176	017176 caenorhabdi	960	6	3.7	32	10	09FV03	09fv03 zea mays su
888	6	4.4	1369	11	063644	063644 rattus norv	961	6	3.7	32	10	09FV00	09fv00 zea luxuria
889	6	4.4	1425	5	09VTP9	09vtp9 drosophila	962	6	3.7	32	10	09FUP9	09fup9 zea luxuria
890	6	4.4	1466	10	09ZUQ3	09zqg3 arabidopsis	963	6	3.7	32	10	09FEB2	09feb2 zea mays su
891	6	4.4	1496	5	09NFX5	09nfx5 drosophila	964	6	3.7	32	10	09FEB1	09feb1 zea mays su
892	6	4.4	1513	4	09NXY3	09nxy3 homo sapien	965	6	3.7	35	2	050052	050052 mycobacteri
893	6	4.4	1534	2	P71227	P71227 escherichia	966	6	3.7	37	4	013528	013528 homo sapien
894	6	4.4	1590	4	09P2N0	09p2n0 homo sapien	967	6	3.7	37	5	09NM39	09nm39 leishmania
895	6	4.4	1626	12	09YK98	09yk98 blackcurran	968	6	3.7	38	2	09RZM5	09rz5 borrelia bu

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969 5 3.7 38 5 018497 018497 caenorhabdi
970 5 3.7 39. 4 09KFE6 09f6c bacillus ha
971 5 3.7 39 4 09Q013 09q13 homo septen
972 5 3.7 41 5 076538 076538 strongyloce
973 5 3.7 42 6 062767 062767 equus caball
974 5 3.7 44 11 004054 004054 rattus norv
975 5 3.7 45 11 097563 097563 mus musculu
976 5 3.7 45 11 09D2R9 09D2R9 mus musculu
977 5 3.7 45 11 09D052 09D052 bovine poly
978 5 3.7 45 13 09DETS 09DETS colutrix co
979 5 3.7 48 5 08GR26 08GR26 aphidius co
980 5 3.7 50 12 09QZJ9 09QZJ9 cavia porce
981 5 3.7 51 12 09J1K8 09J1K8 hepatitis c
982 5 3.7 52 12 096890 096890 hepatitis c
983 5 3.7 52 12 074011 074011 pyrococcus
984 5 3.7 53 5 09U5R8 09U5R8 entodinium
985 5 3.7 53 5 09N706 09N706 leishmania
986 5 3.7 54 9 09T0V8 09T0V8 bacterioph
987 5 3.7 54 12 055469 055469 human herpe
988 5 3.7 54 12 055470 055470 human herpe
989 5 3.7 56 2 099175 099175 porcine ent
990 5 3.7 56 2 09CEV0 09CEV0 bacillus st
991 5 3.7 56 2 09CEV7 09CEV7 lactococcus
992 5 3.7 56 11 09QZK0 09QZK0 cavia porce
993 5 3.7 56 12 056181 056181 human immun
994 5 3.7 56 12 056182 056182 human immun
995 5 3.7 56 12 056183 056183 human immun
996 5 3.7 56 12 056184 056184 human immun
997 5 3.7 56 12 056185 056185 human immun
998 5 3.7 56 12 056187 056187 human immun
999 5 3.7 58 2 0995U2 0995U2 staphylococ
1000 5 3.7 58 10 09LGD9 09LGD9 oryza sativ

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ALIGNMENTS

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RESULT 1
099S07 1 PRELIMINARY: PRT: 163 AA.
AC 099S07;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE STAPHYLOKINASE PRECURSOR.
GN SAK OR SAK158.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iida J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani OI Y.,
RA Takahashi N.K., Sawano T., Inoue K.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuwara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hirayatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003135, BAB43032.1; -.
KW Complete proteome.
SQ SEQUENCE 163 AA; 18520 MW; 413CDAE14BE9FD40 CRC64;

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Query Match 100.0%; Score 136; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2.7e-132;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SSSFDKGRKKGDDASYFEPTGYLMVNTGVDSKGNELSPHYVEPIKPGTTLTKRKI 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db 28 SSSFDKGRKKGDDASYFEPTGYLMVNTGVDSKGNELSPHYVEPIKPGTTLTKRKI 87
Qy 61 EYVENALDATALKEFRVVDPSAKIEVYTDKNKKKEETKSPITEKGFVVDPSLSEHI 120
Db 88 EYVENALDATALKEFRVVDPSAKIEVYTDKNKKKEETKSPITEKGFVVDPSLSEHI 147
Qy 121 KNGFNILTKVYIEKK 136
Db 148 KNGFNILTKVYIEKK 163

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RESULT 2
033929 2 PRELIMINARY: PRT: 136 AA.
AC 033929;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE STAPHYLOKINASE (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Chun H.S., Suk K., Kim S.H.,
RC STRAIN-ATCC 29213;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U77328; AAB84174.1; -.
DR HSSP; P00802; ISSN.
FT NON_TER
SQ SEQUENCE 136 AA; 15551 MW; 79516BBI36CA1A3F CRC64;

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Query Match 73.5%; Score 100; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.7e-95;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 37 NELSPHYVEPIKPGTTLTKRKIEVYEMALDATALKEFRVVDPSAKIEVYTDKNK 96
Db 37 NELSPHYVEPIKPGTTLTKRKIEVYEMALDATALKEFRVVDPSAKIEVYTDKNK 96
Qy 97 KKEETKSPITEKGFVVDPSLSEHIKNGFNILTKVYIEKK 136
Db 97 KKEETKSPITEKGFVVDPSLSEHIKNGFNILTKVYIEKK 136

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RESULT 3
09LC46 3 PRELIMINARY: PRT: 163 AA.
AC 09LC46;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE STAPHYLOKINASE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219005; PubMed=10754251;
RA Horii T., Yokoyama K., Barua S., Odagiri T., Futamura N., Hasegawa T.,
RA Ohta M.;
RT "The staphylokinase gene is located in the structural gene encoding N-
RT acetylmuramyl-L-alanine amidase in methicillin-resistant
RT staphylococcus aureus."
RL FEMS Microbiol. Lett. 185:221-224(2000).
DR EMBL: AB033232; BAA95011.1; -.
KW Kinase.
SQ SEQUENCE 163 AA; 18474 MW; 3DB45E35046029DD CRC64;

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Query Match 71.3%; Score 97; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 3.9e-92;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 KGNELSPHYVEPIKPGTTLTKKEIEYVWALDATAYKFRVVELDPSAKIEVYYDK 94
|||||
DB 62 KGNELSPHYVEPIKPGTTLTKKEIEYVWALDATAYKFRVVELDPSAKIEVYYDK 121
|||||

QY 95 NKKKEETKSPFITKGVVDPDLSEHKNGFNLTITKV 131
|||||
DB 122 NKKKEETKSPFITKGVVDPDLSEHKNGFNLTITKV 158
|||||

RESULT 4
Q9AM04 PRELIMINARY; PRT; 163 AA.

ID Q9AM04
AC Q9AM04;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE STAPHYLOKINASE SAKXH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei W., Xiang H., Tan H.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF332619; AAK11636.1; -
KW Kinase.
SQ SEQUENCE 163 AA; 18509 MW; 0A266B5BEAF65B5A CRC64;

Query Match 68.4%; Score 93; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.2e-88;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YVEPIKPGTTLTKKEIEYVWALDATAYKFRVVELDPSAKIEVYYDKNKKKEETKS 103
|||||
DB 71 YVEPIKPGTTLTKKEIEYVWALDATAYKFRVVELDPSAKIEVYYDKNKKKEETKS 130
|||||

QY 104 FPITEKGVVDPDLSEHKNGFNLTITKVITEK 136
|||||
DB 131 FPITEKGVVDPDLSEHKNGFNLTITKVITEK 163
|||||

RESULT 5
Q9X260 PRELIMINARY; PRT; 245 AA.

ID Q9X260
AC Q9X260;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GCPA PROTEIN.
GN TM1738.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL: AE001812; AAD36803.1; -

DR TIGR; TM1738; -
DR InterPro; IPR000566; Lipocln_cyFABP.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 245 AA; 25865 MW; 1FBAC67841ED2987 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SKGNELLS 41
|||||
DB 219 SKGNELLS 226
|||||

RESULT 6
Q27388 PRELIMINARY; PRT; 56 AA.

ID Q27388
AC Q27388;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 6.4 KDA PROTEIN.
GN MTH1333.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Olu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McQuigall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000897; AAB85811.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 56 AA; 6351 MW; 7709EC4C767AB635 CRC64;

Query Match 5.1%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TLTREK 59
|||||
DB 16 TLTREK 22
|||||

RESULT 7
Q28835 PRELIMINARY; PRT; 90 AA.

ID Q28835
AC Q28835;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE CGMP-GATED RETINAL PHOTORECEPTOR CHANNEL (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Hundal S.P., DiFrancesco D., Mangoni M., Brammar W.J., Conley E.C.;
RL Biochem. Soc. Trans. 21:0-0(1993).

DR EMBL: S65218; AAB27924.1; .
SQ NON_TER 1
FT SEQUENCE 90 AA; 10981 MW; D66843EDBB87830C CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 6; Length 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KKKEETK 102
DB 6 KKKEETK 12

RESULT 8
ID 086603 PRELIMINARY; PRT; 92 AA.
AC 086603;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE COAT PROTEIN (FRAGMENT).
OS Tulip top-breaking virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Polyviruses
OX NCBI_Taxid=32621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93260402; PubMed=8492092;
RA Dekker E.L., Berke A.F., Asjes C.J., Lemmers M.E., Bol J.F.,
RT "Characterization of potyviruses from tulip and lily which cause
flower-breaking.",
RL J. Gen. Virol. 74:881-887(1993).
DR EMBL: S60806; AAB2636.1;
DR InterPro: IPR001592; Pcty_coat.
DR Pfam: PF00767; Pcty_coat; 1.
KW Coat protein.
FT NON_TER 1
SQ SEQUENCE 92 AA; 10891 MW; 752DFCE2E0FC2B10 CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 12; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 VEPPIKP 51
DB 18 VEPPIKP 24

RESULT 9
ID 09K8J5 PRELIMINARY; PRT; 102 AA.
AC 09K8J5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 50S RIBOSOMAL PROTEIN L21.
GN RPLU OR BH3011.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_Taxid=6665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis."

RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS TO 23S RIBOSOMAL RNA IN THE PRESENCE
OF PROTEIN L20 (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L21P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL: AP00517; BAB06730.1;
DR InterPro: IPR001787; Ribosomal_L21p.
DR Pfam: PF00829; Ribosomal_L21p; 1.
DR PROSITE: PS01169; RIBOSOMAL_L21; 1.
KW Complete proteome; Ribosomal protein; rRNA-binding.
SQ SEQUENCE 102 AA; 11350 MW; C929D2F40D75E3FC CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 2; Length 102;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TKVIEK 135
DB 93 TKVIEK 99

RESULT 10
ID 09JEH2 PRELIMINARY; PRT; 114 AA.
AC 09JEH2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RT85;
RX MEDLINE=20148943; PubMed=10684266;
RA Goujon C.P., Schneider V.M., Groft J., Montigny J., Jeanfils V.,
RA Astagneau P., Rozenbaum W., Lot F., Frocraïn-Herchovitch C.,
RA Delphin N., Le Gal F., Nicolas J.-C., Milinkovich M.C., Deny P.,
RT "Phylogenetic Analyses indicate an Atypical Nurse-to-Patient
Transmission of Human Immunodeficiency Virus Type 1.",
RU J. Virol. 74:2525-2532(2000).
CC -1- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE
TRANSCRIPTASE).
DR EMBL: AF125749; AAF72270.1;
DR InterPro: IPR000477; RVTse.
DR Pfam: PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
FT NON_TER 1
SQ SEQUENCE 114 AA; 13140 MW; 2D7D12027706430F CRC64;

Query Match
Best Local Similarity 5.1%; Score 7; DB 12; Length 114;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LTRKITE 61
DB 2 LTRKITE 8

RESULT 11
ID 09KFP3 PRELIMINARY; PRT; 138 AA.
AC 09KFP3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE TRANSPOSASE (14).
GN BH0436.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;


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OC Bacillus/Staphylococcus group; Bacillus.
ON NCBI_TaxID=86665;
RX SEQUENCE FROM N.A.
RP STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; Pubmed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001508; BAB04155.1; -.
KW Complete proteome.
SQ SEQUENCE 138 AA; 16118 MW; FF0BE8229CB5ED82 CRC64;

Query Match 5.1%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 DSKGNEL 39
   |||||
Db 80 DSKGNEL 86

RESULT 12
Q90U35 PRELIMINARY; PRT; 140 AA.
AC Q90U35;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE DNA, COMPLETE GENOME, ISOLATE: TLMV-CBD203.
OS TTV-like mini virus.
OC Viruses: ssDNA viruses; Circoviridae.
OX NCBI_TaxID=93678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLMV-CBD203;
RA Mishiro S.;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TLMV-CBD203;
RA Takahashi K., Iwasa Y., Hijikata M., Mishiro S.;
RT "Identification of a new human DNA virus (TTV-like mini virus: TLMV)
RT immediately related to TTV virus and chicken anemia virus.";
RL Arch. Virol. 0:0-0(1999).
DR EMBL: AB026929; BAA86946.1; -.
SQ SEQUENCE 140 AA; 16573 MW; 607486347884FCE9 CRC64;

Query Match 5.1%; Score 7; DB 12; Length 140;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TTLTKRK 59
   |||||
Db 60 TTLTKRK 66

RESULT 13
Q9WI01 PRELIMINARY; PRT; 154 AA.
AC Q9WI01;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROTEASE (FRAGMENT).
OS Human immunodeficiency virus type 2.
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11709;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEM-13;
RA Rodas B., Holguin A., Soriano V., Dourana M., Mansinho K., Antunes F.,
RA Gonzalez-Lahoz J.M.;
RT "Drug Resistance Mutations in HIV-2-infected Subjects Under
RT Antiretroviral Therapy: Identification of the 151 Multidrug-Resistant
RT Codon in Two Patients.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
DR EMBL: AF139053; AAD37335.1; -.
DR InterPro: IPR001969; Asp-Protease.
DR InterPro: IPR001995; Asp-Proteol.
DR Pfam: PF00077; rvp; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
KW Aspartyl protease; Hydrolase; Protease.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 16821 MW; C47EB4C60405791 CRC64;

Query Match 5.1%; Score 7; DB 12; Length 154;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LTKERIE 61
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Db 124 LTKERIE 130

RESULT 14
Q9NF98 PRELIMINARY; PRT; 181 AA.
AC Q9NF98;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE HYPOTHEICAL 21.8 KDA PROTEIN.
GN PFC1016W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; Pubmed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Felwell T.,
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moulé S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum.";
RL Nature 400:532-538(1999).
DR EMBL: AL034559; CAB92305.1; -.
KW Hypothetical protein.
SQ SEQUENCE 181 AA; 21787 MW; 1F7CD3170DBD70AA CRC64;

Query Match 5.1%; Score 7; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 DKNKKKE 99
   |||||
Db 6 DKNKKKE 12

RESULT 15

```

Q9ACCO
 ID Q9ACCO PRELIMINARY: PRT: 185 AA.
 AC Q9ACCO:
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE OUTER SURFACE PROTEIN PRECURSOR (FRAGMENT).
 GN WSP.
 OS Wolbachia endosymbiont of *Helicoverpa* spp.
 OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales:
 OC Rickettsiaceae: Wolbachiae: Wolbachia.
 OX NCBI_TaxId=118725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cordaux R., Michel-Salzat A., Bouchon D.;
 RT "Wolbachia infection in crustaceans: novel hosts and potential routes
 RT for horizontal transmission";
 RL J. Evol. Biol. 14:237-243(2001).
 DR EMBL; AJ276609; CAC34465.1; -;
 FT NON_TER 1 185
 FT NON_TER 1 185
 SQ SEQUENCE 185 AA; 19928 MW; 026198CA9EDFDE0C CRC64;

Query Match 5.1%; Score 7; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 YKKGDDA 15
 |||||
 Db 24 YKKGDDA 30

Search completed: April 22, 2002, 10:48:48
 Job time: 203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2002, 10:38:39 ; Search time 23.68 seconds
(without alignments)
425.421 Million cell updates/sec

Title: US-09-601-490-1
Perfect score: 715
Sequence: 1 SSSFDKGYKGGDASYFEP.....SEHIKNPCFNLIKVVIEKK 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	100.0	136	17 AAW03071	Wild-type staphylo
2	715	100.0	136	17 AAW03086	Wild-type staphylo
3	715	100.0	136	22 AAB99421	Staphylokinase (Sa
4	715	100.0	136	22 AAB61909	S. aureus staphylo
5	715	100.0	137	14 AAR39150	Staphylokinase SAK
6	712	99.6	136	20 AAY15024	Staphylokinase var
7	711	99.4	136	19 AAW44696	Staphylokinase fro
8	711	99.4	136	20 AAY15022	Staphylokinase var
9	711	99.4	136	20 AAY15025	Staphylokinase var
10	711	99.4	136	20 AAY15016	Staphylokinase var
11	711	99.4	136	20 AAY15021	Staphylokinase var

12	711	99.4	136	22 AAB61908	S. aureus staphylo
13	711	99.4	137	14 AAR39149	Staphylokinase SAK
14	711	99.4	163	12 AAR12137	S. aureus Staphylo
15	711	99.4	163	13 AAR28844	Staphylokinase (SAK
16	711	99.3	136	20 AAY15013	Staphylokinase var
17	709	99.2	136	17 AAW03101	Staphylokinase der
18	709	99.2	136	20 AAY15023	Staphylokinase var
19	709	99.2	136	20 AAY15015	Staphylokinase var
20	709	99.2	136	20 AAY15010	Staphylokinase var
21	709	99.2	136	20 AAY15004	Staphylokinase var
22	709	99.2	136	20 AAY15006	Staphylokinase var
23	708	99.0	136	19 AAW44690	Staphylokinase mut
24	708	99.0	136	19 AAW44693	Staphylokinase mut
25	708	99.0	136	20 AAY15026	Staphylokinase var
26	708	99.0	136	20 AAY15027	Staphylokinase var
27	707	98.9	136	19 AAW44694	Staphylokinase mut
28	707	98.9	136	20 AAY15007	Staphylokinase var
29	707	98.9	136	20 AAY15018	Staphylokinase var
30	707	98.9	136	20 AAY15019	Staphylokinase var
31	707	98.9	136	20 AAY15011	Staphylokinase var
32	706	98.7	136	19 AAW44689	Staphylokinase mut
33	706	98.7	136	19 AAW44692	Staphylokinase mut
34	706	98.7	136	20 AAY15028	Staphylokinase var
35	706	98.7	136	20 AAY15014	Staphylokinase var
36	706	98.7	136	21 AAB01297	Wild type staphylo
37	705	98.6	136	19 AAW44691	Staphylokinase mut
38	705	98.6	136	19 AAW44695	Staphylokinase mut
39	704	98.5	136	20 AAY15041	Staphylokinase var
40	704	98.5	136	20 AAY15020	Staphylokinase var
41	703	98.5	136	20 AAY15012	Staphylokinase var
42	703	98.3	136	17 AAW03079	Staphylokinase der
43	703	98.3	136	17 AAW03078	Staphylokinase der
44	703	98.3	136	17 AAW03082	Staphylokinase der
45	703	98.3	136	17 AAW03076	Staphylokinase der

ALIGNMENTS

RESULT 1
AAW03071
ID AAW03071 standard; protein; 136 AA.

AC AAW03071;

XX 19-FEB-1997 (first entry)

DT Wild-type staphylokinase.

DE Staphylokinase; mutant; mutein; variant; immunogenicity; decrease;

KW derivative; SakSTAR; arterial thrombosis; thrombolytic agent.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 5..6

FT /label= M20_epitope

FT Region 8..10

FT /label= M21_epitope

FT Region 11..14

FT /label= M1_epitope

FT Region 19

FT /label= M22_epitope

FT Region 33..35

FT /label= M2_epitope

FT Region 35..38

FT /label= M3_epitope

FT Region 46..50

FT /label= M4_epitope

FT Region 57..59

FT /label= M5_epitope

FT Region 61..65

FT /label= M6_epitope

prior art

FT	Region	65..69	/label= M7_epitope
FT	Region	74..77	/label= M8_epitope
FT	Region	80..82	/label= M9_epitope
FT	Region	86..88	/label= M10_epitope
FT	Region	93..94	/label= M11_epitope
FT	Region	96..98	/label= M12_epitope
FT	Region	99..100	/label= M13_epitope
FT	Region	99..102	/label= M14_epitope
FT	Region	108..109	/label= M15_epitope
FT	Region	115..119	/label= M16_epitope
FT	Region	119..121	/label= M17_epitope
FT	Region	130	/label= M18_epitope
FT	Region	134..136	/label= M19_epitope
XX	EP721982-A1.		
PN			
XX			
XX	17-JUL-1996.		
PD			
XX			
PF	06-JAN-1995;	95EP-0200023.	
PR			
XX	06-JAN-1995;	95EP-0200023.	
XX			
PA	(COLL)' COLLEN D J.		
PA	(LEUV-) LEUVEN RES & DEV VZW.		
XX			
PI	Collen D;		
XX			
XX	WPI; 1996-322832/33.		
DR			
XX			
PT	New staphylokinase mutants with reduced treating arterial thrombosis		
PT			
XX			
PS	Disclosure; Page 16; 21pp; English.		
XX			
CC	Staphylokinase derivatives showing a compared to wild-type staphylokinase		
CC	are useful as thrombolytic agents to		
CC	are pref. produced by eliminating at		
CC	indicated in the features table. The		
CC	replacing one or more amino acid res		
CC	Ala residue. Mutations are introduced		
CC	mutagenesis on wild-type staphylokin		
CC	lysogenic strain SakSTAR. The presen		
CC	SakSTAR staphylokinase.		
XX			
SQ	Sequence 136 AA;		

Query Match	100.0%;	Score 715;	DB 17;	Length 136;
Best Local Similarity	100.0%;	Pred. No. 1.3e-70;		
Matches 136;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SSSPDKGKKGGDASVFEPTGPLYMNVN7GVDSKGNELLSPHYVEFPKPGTTLTKKI	60	
Db	1	sssfdkgkykkgddasvfeptgplymrvn7vgvdskgnellspHYVEFPKPGTTLTKKI	60	
QY	61	EYVVEWALDATAYKEFRVWELDPSAKIEVYYIDKNKKKEETKSFPIITERGFVVPDLSEHI	120	
Db	61	eyyvewaldataYkefrvvelDpsakievtyydknkkkeetksfPitekfvyvpdlsehi	120	

QY	121	KNPGFNLTQVIEKK	136
Db	121	knpgfnltkvvlekk	136
RESULT	2		
AAW03086			
ID	AAW03086	standard; protein; 136 AA.	
XX	AC	AAW03086;	
XX	XX	19-FEB-1997 (first entry)	
DT	XX	Wild-type staphylokinase.	
DE	XX		
XX	XX	Staphylokinase; mutant; mutein; variant; immunogenicity; decrease; derivative; SakSTAR; arterial thrombosis; thrombolytic agent.	
KW	XX	Staphylococcus aureus.	
KM	XX		
OS	XX		
XX	XX		
XX	XX		
PH	Key	Location/Qualifiers	
FT	Region	5..6	
FT	Region	/label= M20_epitope	
FT	Region	8..10	
FT	Region	/label= M21_epitope	
FT	Region	11..14	
FT	Region	/label= M1_epitope	
FT	Region	19	
FT	Region	/label= M22_epitope	
FT	Region	33..35	
FT	Region	/label= M2_epitope	
FT	Region	35..38	
FT	Region	/label= M3_epitope	
FT	Region	46..50	
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FT	Region	/label= M6_epitope	
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FT	Region	134..136	
FT	Region	/label= M19_epitope	
XX	XX		
XX	XX	WO9621016-A2.	
XX	XX	11-JUL-1996.	
XX	XX		
XX	XX	03-JAN-1996;	96WO-EP000081.
XX	XX	17-NOV-1995;	95JP-0299781.

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PR 06-JAN-1995; 95EP-0200023.
PR 11-JAN-1995; 95US-0371505.
PR 09-JUN-1995; 95EP-0201531.
PR 06-JUL-1995; 95US-0499092.
XX
XX (COLL/) COLLEN D.
XX (LEUV-) LEUVEN RES & DEV VZW.
XX
XX Collen D;
XX
XX WPI; 1996-333991/33.
XX
XX New staphylokinase derivs. having reduced immunogenicity - useful
XX for treating arterial thrombosis
XX
XX Disclosure; Fig 1; 58pp; English.
XX
XX Staphylokinase derivatives showing a reduced immunogenicity as
XX compared to wild-type staphylokinase are claimed. The derivatives
XX are useful as thrombolytic agents to treat arterial thrombosis and
XX are pref. produced by eliminating at least one of the epitopes
XX indicated in the features table. The epitopes are destroyed by
XX replacing one or more amino acid residues in a charge cluster by an
XX Ala residue. Mutations are introduced using site-directed
XX mutagenesis on wild-type staphylokinase genomic DNA from the S.aureus
XX lysogenic strain SakSTAR. The present sequence is that of wild-type
XX SakSTAR staphylokinase.
XX
XX Sequence 136 AA;
SQ

Query Match 100.0%; Score 715; DB 17; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSFDKGYKKGDDASYFEPTGYLMVNVTVGDSKGNELLSPHYVEPIKPGTTLTKEKI 60
Db 1 sssfdkgkykkgddasyfeptgpylmvntvgdskgnellspkyvefpikpgtltkeki 60
QY 61 EYVVEWALDATALYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPFITEKGFVVPDLSEHI 120
Db 61 eyyvewaldataykefrvvelgpsakievtyydknkkkeetksfitekgfvvpdlsehi 120
QY 121 KNPGFNLTWKVIEKK 136
Db 121 knpgfnltkvviekk 136

RESULT 3
AAB99421
ID AAB99421 standard; Protein; 136 AA.
XX
XX AC AAB99421;
XX
XX DT 28-AUG-2001 (first entry)
XX
XX DE Staphylokinase (SakSTAR) primary protein sequence.
XX
XX KW Staphylokinase; Staphylococcus aureus; SakSTAR; T-cell epitope;
XX immunogenic; thrombolytic; acute myocardial infarction; immunogenicity.
XX
XX OS Staphylococcus aureus.
XX
XX PN WO200140281-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 01-DEC-2000; 2000WO-EP12299.
XX
XX PR 02-DEC-1999; 99EP-0204093.
XX
XX PA (THRO-) THROMB-X NV.
XX

PI Warmerdam PAM, Plaisance SDNGH, Collen DJ, De Maeyer MCH;
XX
XX WPI; 2001-374786/39.
XX
XX Reducing immunogenicity of protein (P) by eliminating T cell epitopes
XX in test peptides having amino acid sequence corresponding to (P) and
XX modifying amino acid sequence of (P) according to test peptide
XX modifications.
XX
XX Disclosure; Fig 1; 50pp; English.
XX
XX The present invention describes a method for reducing the immunogenicity
XX of a peptide or protein (I), where (I) can be staphylokinase (SakSTAR)
XX isolated from Staphylococcus aureus. The method involves designing a
XX series of overlapping test peptides having an amino acid sequence
XX corresponding to (I), modifying test peptides which are identified to
XX comprise one or more T-cell epitopes, such that they are reduced or
XX eliminated, and repeating the T-cell eliminating modifications for (I)
XX to produce a modified peptide or protein. Methods from the present
XX invention can be used for the treatment, diagnosis or prophylaxis or
XX for the preparation of a pharmaceutical composition for the treatment,
XX diagnosis or prophylaxis of a human subject. Staphylokinase is used as a
XX potent thrombolytic agent in patients with acute myocardial infarction.
XX The method is useful for reducing cell based immunogenicity of non-human
XX proteins such as streptokinase or antibodies or their fragments, from
XX other species, for diagnostics and treatment of human disease. AAB99400
XX to AAB99449 represent amino acid sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 136 AA;
SQ

Query Match 100.0%; Score 715; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSFDKGYKKGDDASYFEPTGYLMVNVTVGDSKGNELLSPHYVEPIKPGTTLTKEKI 60
Db 1 sssfdkgkykkgddasyfeptgpylmvntvgdskgnellspkyvefpikpgtltkeki 60
QY 61 EYVVEWALDATALYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPFITEKGFVVPDLSEHI 120
Db 61 eyyvewaldataykefrvvelgpsakievtyydknkkkeetksfitekgfvvpdlsehi 120
QY 121 KNPGFNLTWKVIEKK 136
Db 121 knpgfnltkvviekk 136

RESULT 4
AAB61909
ID AAB61909 standard; Protein; 136 AA.
XX
XX AC AAB61909;
XX
XX DT 08-MAY-2001 (first entry)
XX
XX DE S. aureus staphylokinase G34s variant.
XX
XX KW Immunogenicity; staphylokinase; variant; stability.
XX
XX OS Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 34
XX FT /label= G34S
XX FT /note= "wild-type Gly is replaced by Ser"
XX
XX PN WO200104287-A1.
XX
XX PD 18-JAN-2001.
XX
XX PF 06-JUL-2000; 2000WO-DK00371.

```

```
XX 07-JUL-1999; 99DK-0000988.
PR 27-AUG-1999; 99DK-0001196.
PR 02-MAR-2000; 2000DK-0000339.
PR 18-MAY-2000; 2000DK-0000804.
XX
XX (MAXY-) MAXYGEN APS.
PA
XX Halkier T, Pedersen AH, Okkels JS;
PI
XX WPI: 2001-138342/14.
DR
XX
XX Producing polypeptides with altered immunogenicity or improved
PT stability, comprises expressing a diversified nucleotide sequence
PT population and selecting polypeptides with altered immunogenicity or
PT improved stability -
XX
XX Example 1; Page 76; 83pp; English.
PS
XX The invention relates to a method of altering immunogenicity and/or
XX increasing stability of a polypeptide of interest. The method comprises
XX (a) expressing a diversified population of nucleotide sequences encoding
XX a polypeptide of interest; (b) screening the polypeptides expressed for
XX function, immunogenicity and/or stability; and (c) selecting functional
XX polypeptides with altered immunogenicity and/or increased stability. The
XX method is used to improve the properties of polypeptides, in particular
XX to alter the immunogenicity and/or increase the functional in vivo half-
XX life of the polypeptide. The method uses a high throughput system that
XX makes it possible to search several orders of magnitude more polypeptides
XX than is possible by previously known approaches. This enhances the chance
XX of finding the optimal variant from the many thousands of variants that
XX may be produced. The present sequence represents S. aureus staphylokinase
XX variant sequence, used to exemplify the method of the invention.
XX
XX SQ Sequence 136 AA;
XX
XX Query Match 100.0%; Score 715; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-70;
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSSFDKGYKKGGDASVEPTGPLYMNVNVTGVDKGNELLSPHYVEPIKPGTTLTKEKI 60
XX Db 1 sssfdkgkykkgddasyfeptgpylmvntvgvdksgnellshphyvefpkpgttltkeki 60
XX
XX QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYDKNKKKEETKSPITEKGFVVPDLSEHI 120
XX Db 61 eyyvewaldataykefrvveldpsakievtyydknkkkeetksfpitekgfvvpdlsehi 120
XX
XX QY 121 KNPGFNLTIKVVIKK 136
XX Db 121 knpgfnltikvviekk 136
XX
XX RESULT 5
XX AAR39150
XX ID AAR39150 standard; Protein; 137 AA.
XX
XX AC AAR39150;
XX
XX DT 03-DEC-1993 (first entry)
XX
XX DE Staphylokinase SAK-STAR.
XX
XX KW Signal sequence, plasminogen activator; thrombosis; staphylokinase;
XX KW SAK.
XX
XX OS Staphylococcus aureus strain 23.
XX
XX PN W09313209-A.
XX
XX PD 08-JUL-1993.
XX
```

```
PF 28-DEC-1992; 92WO-EF02989.
XX
XX 30-DEC-1991; 91DE-4143279.
PR 22-JUN-1992; 92DE-4220516.
PR 01-DEC-1992; 92DE-4240801.
XX
XX (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
PA
XX Albrecht S, Behnke D, Guehrs K, Hartmann M, Schlott B;
PI
XX WPI: 1993-227325/28.
DR N-PSDB; AARQ44270.
XX
XX Staphylo-kinase (SAK) sequences lacking sequences for signal
PT peptide(s) - for prodn. of proteins used as plasminogen
PT activators in thrombosis treatment, and monoclonal antibodies
PT against SAK
XX
XX Claim 3; Fig 3; 99pp; German.
PS
XX DNA encoding SAK lacking the signal peptide, is expressed
XX intracellularly. This avoids the problem of fast degradation of the
XX polypeptides or destruction of the host when expressed into the
XX medium or into the periplasm respectively. High expression is
XX possible and the chemically induced overprodn. is easy to handle.
XX Also, the prods. are homogeneous.
XX SAK-polypeptide derivs. are plasminogen activators for the
XX treatment of thrombosis.
XX
XX SQ Sequence 137 AA;
XX
XX Query Match 100.0%; Score 715; DB 14; Length 137;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-70;
XX Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSSFDKGYKKGGDASVEPTGPLYMNVNVTGVDKGNELLSPHYVEPIKPGTTLTKEKI 60
XX Db 2 sssfdkgkykkgddasyfeptgpylmvntvgvdksgnellshphyvefpkpgttltkeki 61
XX
XX QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYDKNKKKEETKSPITEKGFVVPDLSEHI 120
XX Db 62 eyyvewaldataykefrvveldpsakievtyydknkkkeetksfpitekgfvvpdlsehi 121
XX
XX QY 121 KNPGFNLTIKVVIKK 136
XX Db 122 knpgfnltikvviekk 137
XX
XX RESULT 6
XX AAY15024
XX ID AAY15024 standard; Protein; 136 AA.
XX
XX AC AAY15024;
XX
XX DT 03-NOV-1999 (first entry)
XX
XX DE Staphylokinase variant SakSTAR (V132L).
XX
XX KW Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
XX KW SakSTAR (V132L); anti-thrombotic; fibrinolytic; cardiac; veterinary;
XX KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
XX KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 132
XX PN /note= "Wild type Val is substituted by Leu"
XX PD W09940198-A2.
XX
```



```
PR 04-FEB-1998; 98EP-0200323.
XX (COLL/) COLLEN D J.
PA (LEUV-) LEUVEN RES & DEV VZW.
XX Collen DJ;
XX WPI; 1999-508504/42.
XX Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis
XX Claim 7; Page -: 101pp; English.
XX The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteine modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in figure 1.
XX Sequence 136 AA;
SQ
Query Match 99.4%; Score 711; DB 20; Length 136;
Best Local Similarity 99.3%; Pred. No. 3.6e-70;
Matches 135; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSSFDKGYKKGDDASYFEPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKEKI 60
DB 1 sssfdkgykkgddasyfeptgplymnvntgvdskgnellsphyvefpikpgtlttkeki 60
QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPFITEKGFVVVDLSEHI 120
DB 61 eyvvewaldataykefrvveldpsakievtyydknkkkeetksfpitekgyfvvvpdlsehi 120
QY 121 KNPGFNLTIKVIEKK 136
DB 121 knpgfnlitzkviekk 136
RESULT 9
AAY15025
ID AAY15025 standard; Protein; 136 AA.
XX AAY15025;
XX 03-NOV-1999 (first entry)
XX Staphylokinase variant SakSTAR (V132T).
XX Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KW SakSTAR (V132T); anti-thrombotic; fibrinolytic; cardiant; veterinary;
KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX Staphylococcus aureus.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 132 /note= "wild type val is substituted by Thr"
FT FT
XX W09940198-A2.
```

```
XX 12-AUG-1999.
XX 04-FEB-1999; 99WO-EP00748.
XX 06-FEB-1998; 98EP-0200365.
XX 04-FEB-1998; 98EP-0200323.
XX (COLL/) COLLEN D J.
PA (LEUV-) LEUVEN RES & DEV VZW.
XX Collen DJ;
XX WPI; 1999-508504/42.
XX Staphylokinase derivatives with reduced immunogenicity, used for,
PT e.g. treatment of arterial thrombosis
XX Claim 7; Page -: 101pp; English.
XX The present sequence is a specifically claimed Staphylokinase SakSTAR
CC variant. This variant has one aminoacid that has been substituted
CC by another aminoacid that reduces the reactivity with monoclonal
CC antibodies and absorption of SakSTAR-specific antibodies from plasma
CC of patients treated with staphylokinase. The derivatives can also be
CC substituted with cysteine modified with PEG to maintain the specific
CC activity and significantly reduce the plasma clearance. They have
CC altered immunogenicity without markedly reducing the specific activity.
CC This sequence has anti-thrombotic, cardiant activity and a fibrinolytic
CC potency in human plasma. The new staphylokinase derivatives are used
CC for treatment of arterial thrombosis, especially myocardial infarction.
CC The compositions can be used in human or veterinary practice.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the Staphylococcus aureus wild type staphylokinase sequence
CC given in figure 1.
XX Sequence 136 AA;
SQ
Query Match 99.4%; Score 711; DB 20; Length 136;
Best Local Similarity 99.3%; Pred. No. 3.6e-70;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SSSFDKGYKKGDDASYFEPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKEKI 60
DB 1 sssfdkgykkgddasyfeptgplymnvntgvdskgnellsphyvefpikpgtlttkeki 60
QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPFITEKGFVVVDLSEHI 120
DB 61 eyvvewaldataykefrvveldpsakievtyydknkkkeetksfpitekgyfvvvpdlsehi 120
QY 121 KNPGFNLTIKVIEKK 136
DB 121 knpgfnlitzkviekk 136
RESULT 10
AAY15016
ID AAY15016 standard; Protein; 136 AA.
XX AAY15016;
XX 03-NOV-1999 (first entry)
XX Staphylokinase variant SakSTAR (V132A).
XX Staphylokinase; variant; immunogenic; specificity; derivative; cysteine;
KW SakSTAR (V132A); anti-thrombotic; fibrinolytic; cardiant; veterinary;
KW Staphylococcus aureus; myocardial infarction; arterial thrombosis;
KW monoclonal antibody; polyethylene glycol; PEG; plasma clearance.
XX Staphylococcus aureus.
OS Synthetic.
```



```

XX 08-MAY-2001 (first entry)
XX S. aureus staphylokinase mature protein sequence.
XX
XX Immunogenicity; staphylokinase; variant; stability.
XX
XX Staphylococcus aureus.
XX
XX WO200104287-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-DK00371.
XX
XX 07-JUL-1999; 99DK-0000988.
XX
XX 27-AUG-1999; 99DK-0001196.
XX
XX 02-MAR-2000; 2000DK-0000339.
XX
XX 18-MAY-2000; 2000DK-0000804.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Halkier T, Pedersen AH, Okkels JS;
XX
XX WPI; 2001-138342/14.
XX
XX N-PSDB; AAC85112.
XX
XX Producing polypeptides with altered immunogenicity or improved
XX stability, comprises expressing a diversified nucleotide sequence
XX population and selecting polypeptides with altered immunogenicity or
XX improved stability -
XX
XX Example 1; Page 75; 83pp; English.
XX
XX The invention relates to a method of altering immunogenicity and/or
XX increasing stability of a polypeptide of interest. The method comprises
XX (a) expressing a diversified population of nucleotide sequences encoding
XX a polypeptide of interest; (b) screening the polypeptides expressed for
XX function, immunogenicity and/or stability; and (c) selecting functional
XX polypeptides with altered immunogenicity and/or increased stability. The
XX method is used to improve the properties of polypeptides, in particular
XX to alter the immunogenicity and/or increase the functional in vivo half-
XX life of the polypeptide. The method uses a high throughput system that
XX makes it possible to search several orders of magnitude more polypeptides
XX than is possible by previously known approaches. This enhances the chance
XX of finding the optimal variant from the many thousands of variants that
XX may be produced. The present sequence represents S. aureus staphylokinase
XX mature protein sequence, used to exemplify the method of the invention.
XX
XX Sequence 136 AA;
XX
XX Query Match 99.4%; Score 711; DB 22; Length 136;
XX Best Local Similarity 99.3%; Pred. No. 3.6e-70;
XX Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 SSSFDKGYKKGDDASYEPTGPILMVNVTVGDSKGNELLSPHYVEFPDKGTTLTKEKI 60
XX
XX Db 1 sssfdkgykkgddasyeftp-gpyilmvntvgdgknellsphyvvefpdkp9ttltkeki 60
XX
XX Qy 61 EYVWEALDAYAYKEFRVVELDPSAKIEVTVYDKNKKKEETKSFPITEKGFVVPDLSEHI 120
XX
XX Db 61 eyvwealdayakefrvveildpsakievtydyknkkkeetksfpitekgfvvpdlsehi 120
XX
XX Qy 121 KNPGFNLTIKVVIIEKK 136
XX
XX Db 121 knpgfnltikvviiekk 136
XX
XX RESULT 13
XX AAR39149
XX ID AAR39149 standard; Protein; 137 AA.
XX

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XX SAK; protein production.
XX Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..27
XX Protein /label= signal peptide
XX /label= staphylokinase
XX JP0309595-A.
XX PN
XX PD
XX 24-APR-1991.
XX PF 11-SEP-1989; 89JP-0234874.
XX PR 11-SEP-1989; 89JP-0234874.
XX (TAIS) TAISHO PHARMACEUT KK.
XX WPI; 1991-167039/23.
XX DR N-PSDB; AAQ11813.
XX
XX Prepn. of peptide(s) - by construction of expression
XX vector, transformation of E.coli etc., culturing to secrete
XX peptide(s) and collecting peptide(s)
XX Example; Fig 3; 15pp; Japanese.
XX
XX The first 79 residues of this sequence form part of a fusion
XX protein with somatomedin C. A synthetic construct encoding the
XX SAK-SMC fusion is used to transform E.coli or Bacillus subtilis.
XX The SAK signal peptide directs extracellular secretion of the
XX somatomedin C.
XX See also AAQ11814.
XX
XX Sequence 163 AA;
SQ

Query Match 99.4%; Score 711; DB 12; Length 163;
Best Local Similarity 99.3%; Pred. No. 4.6e-70;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SSFDDKGYKKGDDASVFETGPGYLMVNVTCVDSKGNELLSPHYVEPIKPGTTLTKEKI 60
DB 28 SSFDDKGYKKGDDASVFETGPGYLMVNVTCVDSKGNELLSPHYVEPIKPGTTLTKEKI 87
QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTVYDKNKKKEETKSPITEKGFVVPDLSEHI 120
DB 88 EYVVEWALDATAYKEFRVVELDPSAKIEVTVYDKNKKKEETKSPITEKGFVVPDLSEHI 147
QY 121 KNPGFNLITKVVIEKK 136
DB 148 KNPGFNLITKVVIEKK 163

RESULT 15
ID AAR28844
XX AAR28844 standard; Protein; 163 AA.
XX AC AAR28844;
XX 13-JAN-1993 (first entry)
XX DE Staphylokinas (SAK).
XX KW Staphylokinase; thrombosis; fibrinogen; plasminogen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX Peptide 1..27

FT Protein /label= sig_peptide
FT 28..163 /label= mat_protein
XX
XX WO9211356-A.
XX PN
XX PD 09-JUL-1992.
XX PF 17-DEC-1991; 91WO-JP01722.
XX PR 17-DEC-1990; 90JP-0411063.
XX (HONS) YAKULT HONSHA KK.
XX Hashimoto S, Matsumoto T, Matsuo O, Onoue M, Sakai M;
XX Sako T, Sansawa H, Shimura K, Shishido Y, Watanabe T;
XX Yokokura T;
XX WPI; 1992-250079/30.
XX
XX Thrombolytic peptide SAK-11 derived from staphylokinase - useful
XX as a plasminogen activator for treating thrombosis
XX
XX Disclosure; Page 16; 26pp; Japanese.
XX
XX SAK-11 (AAR25468) is derived from its precursor, staphylokinase (SAK)
XX - represented in AAR28844, by tryptic cleavage of its 10 N-terminal
XX amino acid residues. SAK-11 is useful as the active agent in an
XX injectable treatment for thrombosis. Thrombolytic activity is
XX demonstrated using a rabbit jugular vein thrombosis model. A clear
XX decrease in fibrinogen is observed upon application of 0.9 mg SAK-11/
XX kg. Plasminogen activation is superior to that of SAK (no specific
XX data given). Furthermore, SAK-11 has very low antigenicity as shown
XX in a PCA study, against streptokinase and egg albumin controls, in
XX BALB/c mice.
XX
XX Sequence 163 AA;
SQ

Query Match 99.4%; Score 711; DB 13; Length 163;
Best Local Similarity 99.3%; Pred. No. 4.6e-70;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SSFDDKGYKKGDDASVFETGPGYLMVNVTCVDSKGNELLSPHYVEPIKPGTTLTKEKI 60
DB 28 SSFDDKGYKKGDDASVFETGPGYLMVNVTCVDSKGNELLSPHYVEPIKPGTTLTKEKI 87
QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTVYDKNKKKEETKSPITEKGFVVPDLSEHI 120
DB 88 EYVVEWALDATAYKEFRVVELDPSAKIEVTVYDKNKKKEETKSPITEKGFVVPDLSEHI 147
QY 121 KNPGFNLITKVVIEKK 136
DB 148 KNPGFNLITKVVIEKK 163

Search completed: April 22, 2002, 10:41:30
Job time: 171 sec

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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:40:19 ; Search time 12.47 Seconds
(without alignments)
245.425 Million cell updates/sec

Title: US-09-601-490-1
Perfect score: 715
Sequence: 1 SSSFDGKGYKGGDASYFEP.....SEHIKNPGFNLTIKVIEKK 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	100.0	136	1 US-08-371-505-2	Sequence 2, Appl1
2	715	100.0	136	2 US-08-784-971-5	Sequence 5, Appl1
3	715	100.0	137	1 US-08-256-261-6	Sequence 6, Appl1
4	715	100.0	137	3 US-08-852-299-6	Sequence 6, Appl1
5	711	99.4	137	1 US-08-256-261-4	Sequence 4, Appl1
6	711	99.4	137	3 US-08-852-299-4	Sequence 4, Appl1
7	705	98.6	163	1 US-08-075-545-1	Sequence 1, Appl1
8	695	97.2	137	1 US-08-256-261-2	Sequence 2, Appl1
9	695	97.2	137	3 US-08-852-299-2	Sequence 2, Appl1
10	695	97.2	163	1 US-08-256-261-17	Sequence 17, Appl1
11	695	97.2	163	3 US-08-852-299-17	Sequence 17, Appl1
12	692	96.8	137	1 US-08-256-261-14	Sequence 14, Appl1
13	692	96.8	137	3 US-08-852-299-14	Sequence 14, Appl1
14	689	96.4	137	1 US-08-256-261-12	Sequence 12, Appl1
15	689	96.4	137	3 US-08-852-299-12	Sequence 12, Appl1
16	653	91.3	126	1 US-08-075-545-2	Sequence 2, Appl1
17	643	89.9	127	1 US-08-256-261-8	Sequence 8, Appl1
18	643	89.9	127	3 US-08-852-299-8	Sequence 8, Appl1
19	620	86.7	123	1 US-08-256-261-10	Sequence 10, Appl1
20	620	86.7	123	3 US-08-852-299-10	Sequence 10, Appl1
21	74	10.3	592	4 US-09-000-145-6	Sequence 6, Appl1
22	73.5	10.3	252	4 US-09-251-645-13	Sequence 13, Appl1
23	73	10.2	14	2 US-08-934-222-23	Sequence 23, Appl1
24	73	10.2	14	2 US-08-933-402-23	Sequence 23, Appl1
25	73	10.2	14	2 US-09-207-621-23	Sequence 23, Appl1
26	73	10.2	14	2 US-08-532-818-23	Sequence 23, Appl1
27	73	10.2	14	3 US-09-231-797-23	Sequence 23, Appl1

28	73	10.2	14	3 US-08-934-224-23	Sequence 23, Appl1
29	73	10.2	14	3 US-08-933-843-23	Sequence 23, Appl1
30	73	10.2	14	4 US-08-934-223-23	Sequence 23, Appl1
31	73	10.2	14	4 US-09-413-492-23	Sequence 1, Appl1
32	73	10.2	770	1 US-08-525-654A-1	Sequence 3, Appl1
33	73	10.2	771	1 US-08-525-654A-3	Sequence 10, Appl1
34	73	10.2	2509	1 US-08-469-005A-10	Sequence 2, Appl1
35	73	10.2	2511	4 US-09-261-907-2	Sequence 29, Appl1
36	70.5	9.9	706	1 US-08-339-152A-29	Sequence 4, Appl1
37	70.5	9.9	706	2 US-08-007-999B-4	Sequence 4, Appl1
38	70.5	9.9	706	2 US-08-689-276A-4	Sequence 8, Appl1
39	69	9.7	423	1 US-08-476-008-8	Sequence 8, Appl1
40	69	9.7	423	1 US-08-306-063-8	Sequence 8, Appl1
41	69	9.7	423	1 US-08-833-485-8	Sequence 8, Appl1
42	69	9.7	423	4 US-09-137-440-8	Sequence 8, Appl1
43	69	9.7	423	5 PCT-US91-06148A-8	Sequence 7, Appl1
44	69	9.7	427	4 US-09-243-374-7	Patent No. 5310667
45	69	9.7	427	6 5310667-7	

ALIGNMENTS

RESULT 1
US-08-371-505-2
; Sequence 2, Application US/08371505
; Patent No. 5695754
; GENERAL INFORMATION:
; APPLICANT: COLLEN, DESIRE
; TITLE OF INVENTION: STAPHYLOKINASE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEBB ZIESENHEIM BRUENING LOGSDON ORKIN & HANSON, P.C.
; STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
; CITY: PITTSBURGH
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 15222-2363
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,505
; FILING DATE: 11 JAN 1995
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-371-505-2

Query Match 100.0%; Score 715; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.4e-78;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SSSFDGKGYKGGDASYFEP	TGPLYMNVGTGVDKGNELLSPHYVEPIKPGTTLTKEKI	60
Db	1	SSSFDGKGYKGGDASYFEP	TGPLYMNVGTGVDKGNELLSPHYVEPIKPGTTLTKEKI	60
QY	61	EYVEWALDATAATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI	120	
Db	61	EYVEWALDATAATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI	120	
QY	121	KNPGFNLIITKWIEKK	136	
Db	121	KNPGFNLIITKWIEKK	136	

US-08-075-545-1
: Sequence 1, Application US/08075545
: Patent No. 5475089
: GENERAL INFORMATION:
: APPLICANT: MATSUO, Osamu; SAKAI, Masashi; SHIMURA,
: APPLICANT: KISAKU; SANSAWA, Hiroshi; WATANABE,
: APPLICANT: Tsunekazu; MATSUMOTO, Tsuneo; SHISHIDO,
: APPLICANT: Yoshiyuki; HASHIMOTO, Shusuke; YOKOKURA,
: APPLICANT: Teruo; ONOUE, Masaharu; SAKO, Tomoyuki
: TITLE OF INVENTION: THROMBOLYTIC AGENT
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: KECK, MAHIN & CATE
; STREET: P.O. BOX 06110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606-0110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/PC DOS
; SOFTWARE: DOS Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,545
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/01722
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleit, Martin; Gollin, Michael A.
; REGISTRATION NUMBER: 16,900; 31,957
; REFERENCE/DOCKET NUMBER: 47004-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 789-3400
; TELEFAX: (202) 789-1158
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-545-1

Query Match      98.68; Score 705; DB 1; Length 163;
Best Local Similarity 98.5%; Pred. No. 3e-77;
Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSFDKGYKKGGDASVFPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKRKI 60
   |||||||
DB 28 SSSFDKGYKKGGDASVFPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKRKI 87
   |||||||

QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI 120
   |||||||
DB 88 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI 147
   |||||||

QY 121 KNPGFNLTITKVIEKK 136
DB 148 KNPGFNLTITKVIEKK 163

RESULT 8
US-08-256-261-2
; Sequence 2, Application US/08256261
; Patent No. 5801037
; GENERAL INFORMATION:
; APPLICANT: Behnke, Detlef
; APPLICANT: Schlott, Bernhard
; APPLICANT: Albrecht, Sybille
; APPLICANT: G hrs, Karl-Heinz
; APPLICANT: Hartmann, Manfred
; TITLE OF INVENTION: Expression of signal-peptide-free
; TITLE OF INVENTION: staphylokinases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,299
; FILING DATE: 17-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,261
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-299-2

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,261
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-256-261-2

Query Match      97.2%; Score 695; DB 1; Length 137;
Best Local Similarity 97.8%; Pred. No. 3.7e-76;
Matches 133; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSSFDKGYKKGGDASVFPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKRKI 60
   |||||||
DB 2 SSSFDKGYKKGGDASVFPTGPLYMNVNVTGVDKGNELLSPHYVEFPKPGTTLTKRKI 61
   |||||||

QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI 120
   |||||||
DB 62 EYVVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSPITEKGFVVPDLSEHI 121
   |||||||

QY 121 KNPGFNLTITKVIEKK 136
DB 122 KNPGFNLTITKVIEKK 137

RESULT 9
US-08-852-299-2
; Sequence 2, Application US/08852299
; Patent No. 6010897
; GENERAL INFORMATION:
; APPLICANT: Behnke, Detlef
; APPLICANT: Schlott, Bernhard
; APPLICANT: Albrecht, Sybille
; APPLICANT: G hrs, Karl-Heinz
; APPLICANT: Hartmann, Manfred
; TITLE OF INVENTION: Expression of signal-peptide-free
; TITLE OF INVENTION: staphylokinases
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,299
; FILING DATE: 17-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,261
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-299-2

```


Db	62	EYVVEALDATAYPEFRVVELOPSAKIEVYYDKNKKKEETKSFPITEKGFVVPOLSEHI	121
QY	121	KNPGFNLITKWIEKK	136
Db	122	KNPGFNLITKWIEKK	137

RESULT 15

```

US-08-852-299-12
: Sequence 12, Application US/08852299
: Patent No. 6010897
: GENERAL INFORMATION:
: APPLICANT: Behnke, Detlef
: APPLICANT: Schlott, Bernhard
: APPLICANT: Albrecht, Sybille
: APPLICANT: G hrs, Karl-Heinz
: APPLICANT: Hartmann, Manfred
: TITLE OF INVENTION: Expression of signal-peptide-free
: TITLE OF INVENTION: staphylokinases
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/852,299
: FILING DATE: 17-MAY-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/256,261
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 137 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-852-299-12

```

Query Match	96.4%	Score 689;	DB 3;	Length 137;
Best Local Similarity	97.1%	Pred. No. 1.9e-75;		
Matches 132;	Conservative	0;	Mismatches 4;	Indels 0;
Gaps	0;			

QY	1	SSSFDKGGKGGDDASFEPTGPYLMVNVTVGDSKGNELLSPHYVEPIKPGTTLTKEKI	60
Db	2	SSSFDKGGKGGDDASFEPTGPYLVNVTVGDSKGNELLSPRYVEPIKPGTTLTKEKI	61
QY	61	EYYVEWALDATAYAKEFRVVELDPSAKTEVTVYDKNKKKEETKSPITEKGFVPDLSHI	120
Db	62	EYYVEWALDATAYAKEFRVVELDPSAKTEVTVYDKNKKKEETKSPITEKGFVPDLSHI	121
QY	121	KNPGFNLTIKVWIEKK	136
Db	122	KNPGFNLTIKVWIEKK	137

Search completed: April 22, 2002, 10:41:49
Job time: 90 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2002, 10:38:39 ; Search time 14.37 Seconds
(without alignments)
720.928 Million cell updates/sec

Title: US-09-601-490-1
Perfect score: 715
Sequence: 1 SSSFDKGYKKGDDASYFEP.....SEHIKNPGFNLTITKVVIEKK 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	99.4	163	1 PRSAK	staphylokinase - p
2	695	97.2	163	2 S02330	staphylokinase - p
3	87	12.2	348	2 B69790	hypothetical prote
4	84.5	11.8	172	1 WNVZTH	BamHI-ORF13 prote
5	83	11.6	611	2 D72275	conserved hypothet
6	80.5	11.3	158	2 B71192	hypothetical prote
7	80.5	11.3	3097	2 T00021	DN-cadherin - frui
8	78.5	11.0	324	2 E64487	hypothetical prote
9	78	10.9	350	2 C56118	vetispiradiene syn
10	77.5	10.8	441	1 ITBPT4	DNA topoisomerase
11	77	10.8	559	2 T08174	sesquiterpene cycl
12	77	10.8	608	2 I53269	prolactin receptor
13	76.5	10.7	289	2 C69349	conserved hypothet
14	76.5	10.7	506	1 PIWUB4	LI protein - bovin
15	76	10.6	252	2 E86822	hypothetical prote
16	75.5	10.6	327	2 C35411	alkanal monooxygen
17	75	10.5	576	2 G72277	NH(3)-dependent NA
18	74.5	10.4	2512	1 XYCHFA	fatty-acid synthas
19	74	10.3	233	2 T24714	hypothetical prote
20	74	10.3	233	2 D69407	medium-chain acyl-
21	74	10.3	256	2 T24713	hypothetical prote
22	74	10.3	298	2 H64402	molybdopterin bios
23	74	10.3	462	2 T01732	UTP-glucose glucos
24	74	10.3	480	2 B85014	probable flavonol
25	74	10.3	552	2 D82878	phosphomannomutase
26	74	10.3	610	2 A34631	lactogen receptor
27	74	10.3	610	2 A36116	prolactin receptor
28	73.5	10.3	430	2 T04668	phosphoserine tran
29	73.5	10.3	431	2 E96671	hypothetical prote

30	73.5	10.3	764	2 T39878	hypothetical prote
31	73.5	10.3	1536	2 E72310	hypothetical prote
32	73	10.2	237	2 C84976	tRNA (guanine-N1-)
33	73	10.2	263	2 C65044	hypothetical prote
34	73	10.2	470	2 B96637	hypothetical prote
35	73	10.2	2505	1 XYRTFA	fatty-acid synthas
36	73	10.2	2509	2 G01880	fatty-acid synthas
37	73	10.2	4969	2 A37113	ryanodine receptor
38	72.5	10.1	374	2 C85791	hypothetical prote
39	72.5	10.1	374	2 B64941	probable choline m
40	72.5	10.1	430	2 B84946	peptidylprolyl iso
41	72.5	10.1	584	2 C70425	transporter (extra
42	72.5	10.1	935	2 T50774	probable translati
43	72.5	10.1	1043	2 F86504	isoleucyl-tRNA syn
44	72.5	10.1	1043	2 E72118	isoleucine--tRNA 1
45	72	10.1	417	2 A75563	2-oxoglutarate deh

ALIGNMENTS

RESULT 1

PRSAK

staphylokinase - phage S phi-C

C:Species: phage S phi-C

A:Note: host Staphylococcus aureus

C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 28-May-1999

C:Accession: A00995

R:Sako, T.; Tsuchida, N.

Nucleic Acids Res. 11, 7679-7693, 1983

A:Title: Nucleotide sequence of the staphylokinase gene from Staphylococcus aureus.

A:Reference number: A00995; MUID:84069795

A:Accession: A00995

A:Molecule type: DNA

A:Residues: 1-163 <SAK>

A:Cross-references: GB:X00127; NID:g47425; PIDN:CAA24957.1; PID:g758303

C:Comment: Although it has no intrinsic proteolytic activity, this secreted protein i

cture of plasminogen is thought to expose the plasmin active site.

C:Comment: The designation of staphylokinase as synonomous with Staphylococcal aureus

C:Genetics:

A:Gene: sak

C:Superfamily: phage S phi-C staphylokinase

C:Keywords: plasminogen activator

Query Match 99.4%; Score 711; DB 1; Length 163;
Best Local Similarity 99.3%; Pred. No. 7.8e-57;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSFDKGYKKGDDASYFEP TGPYLMVNTGVDKSGNELLSPHYVEFPKPGTTLTKKI 60

Db 28 SSSFDKGYKKGDDASYFEP TGPYLMVNTGVDKSGNELLSPHYVEFPKPGTTLTKKI 87

QY 61 EYVVEWALDATAYKEFRVWELDSPAKIEVTYYDKNKKKEETKSPITEKGVVPDLSEHI 120

Db 88 EYVVEWALDATAYKEFRVWELDSPAKIEVTYYDKNKKKEETKSPITEKGVVPDLSEHI 147

QY 121 KNPGFNLTITKVVIEKK 136

Db 148 KNPGFNLTITKVVIEKK 163

RESULT 2

S02330

staphylokinase - phage P42D

C:Species: phage P42D

A:Note: host Staphylococcus aureus

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-Aug-1999

C:Accession: S02330; S45654

R:Behnke, D.; Gerlach, D.

Mol. Gen. Genet. 210, 528-534, 1987

A:Title: Cloning and expression in Escherichia coli. Bacillus subtilis, and Streptoco

A:Reference number: S02330; MUID:88121731

A:Accession: S02330
A:Molecule type: DNA
A:Residues: 1-163 <BEH>
A:Cross-references: EMBL:X06603; NID:q46676; PIDN:CAA29822.1; PID:q758275
R:Gase, A.; Birch-Hirschfeld, E.; Guehrs, K.H.; Hartmann, M.; Vetterman, S.; Damaschun, Eur. J. Biochem. 223, 303-308, 1994
A:Title: The thermostability of natural variants of bacterial plasminogen-activator star
A:Reference number: S45654; MUID:94307274
A:Accession: S45654
A:Molecule type: protein
A:Residues: 28-163 <GAS>
C:Genetics:
A:Gene: sak
C:Superfamily: phage S phi-C staphylokinase

Query Match 97.2%; Score 695; DB 2; Length 163;
Best Local Similarity 97.8%; Pred. No. 2.1e-55;
Matches 133; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSFDFGKGYKKGDDASYEFTPGYLMVNVGTGVDKGNELSSHYHVFPIKPGTTLTKKEI 60
|||||
Db 28 SSSFDGKGYKKGDDASYEFTPGYLMVNVGTGVDKGNELSSHYHVFPIKPGTTLTKKEI 87
|||||
QY 61 EYVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSFPIKPGTTLTKKEI 120
|||||
Db 88 EYVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSFPIKPGTTLTKKEI 147
|||||
QY 121 KNPGFNLTIKVVIK 136
|||||
Db 148 KNPGFNLTIKVVIK 163
|||||

RESULT 3
B69790
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
A:Accession: B69790
R:Gase, A.; Bron, S.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A.; Schlegel, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
keuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Togonoi, A.; Tosato, V.; Uchiyama,
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
C:Accession: B69790
C:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-348 <KUN>
C:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12445.1; PID:el182605;
Experimental source: strain 168
C:Genetics:
A:Gene: ydJN

Query Match	12.2%	Score 87;	DB 2;	Length 348;
Best Local Similarity	26.5%;	Pred. No. 2.1;		
Matches	31; Conservative	18; Mismatches	34; Indels	34; Gaps
QY	5 DKGYKKGGDASYEETGCGPYLMVNWTVGDSCGNELLSPHYVEFFIKPGCTITLTKKIEYIV	64		
	: : :			
Dd	27 DKG-KEAARDVSNVTESGDELLVITDTD-----LLTKY-----ENDKVIHEKRLTSP	75		

QY	8	KYKCGDDASVEETPG	-----PYLMVNTGVDSKGN	-----ELLSPHYVEFP	IKP	51
Db	163	RYILGDGAINVSGQGVAAKTSYTF	FLVKSMIETSSKNDGDLRELREAR	YII	NVKG	222
QY	52	GTTLTTKKIEVYEWALDATA	YAKE-FRVVELDPSAKIEVYYDK	NKKKEETKSF	TEKG	110
Db	223	ESULLFDLRIS-FKEWYSERKEK	WDMETRVUGIEPKPFENVA	FY-----	APSR	369

```

QY      65  EWALDATAKFRVVELDPSAKIEVTVYDKNKKKEETKSPITEKGFVVPDLSEHIK 121
      :|||      :|||      :|||      :|||      :|||      :|||
Db      76  AFALD-----KQOVLYYTGNQNEWRFLKL-----DLKSHKK 109

      4
RESULT
WMV2TH
BamHI-ORF13 protein - fowlpox virus (isolate HP-438 [Munich]) (fragment)
C:Species: fowlpox virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2
C:Accession: D30087
R:Tomey, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A:Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fra
A:Reference number: JT0442; MUID:88229622
A:Accession: D30087
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-172 <TOM>
A:Cross-references: GB:D00295; NID:g221380; PIDN:BAA00209.1; PID:g221400
C:Superfamily: fowlpox virus BamHI-ORF13 protein
C:Keywords: early protein

```

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Query Match      11.8%; Score 84.5; DB 1; Length 172;  
Best Local Similarity 25.2%; Pred. No. 1.5;  
Matches 31; Conservative 19; Mismatches 36; Indels 37; Gaps  
  
Qy    43 HYVEFPIKPGTITLKEKI-EYVWEVALDATA-----YKEFRV---VEL 80  
       || | :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db    38 HYLCKPIHTAANTSISKIVLLIEYGADINSEGDGANGKYPTHYAMKVYDPFKLIKVL 9  
       || | | | | | | | | | | | | | | | | | | | |  
  
Qy    82 DPSAKIETVVYDKNKKKETKSFPITEKGFFVPDLSEHIKNPGNL-----TKVV 13  
       | | | | | | | | | | | | | | | | | | | | |  
Db    98 DHGA-----DINKQSULTNTSPLETFRFTIDDLLDYIIISRGANIKINEEWYEYITRII 15  
       || | | | | | | | | | | | | | | | | | | | |  
  
Qy    133 IEK 135  
        :| :|  
Db   151 LER 153
```

RESULT 5
D72275 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: D72275
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria
A:Reference number: A77200; MUID:99287316
A:Accession: D72275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-611 <ARN>
A:Cross-references: GB:AE001781; GB:AE000512; NID:g4981810; PIDN:AAD36331
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1257

Query Match	11.6%;	Score 83;	DB 2;	Length 611;
Best Local Similarity	21.5%;	Pred. No. 9, 3;		
Matches	28;	Conservative 27;	Mismatches 45;	Indels 30; Gaps
QY	8	KYKGGDASAEFTG-----PYLMVNVTGVDKGN-----	ELLSPHYVEFPK 51	
Db	163	RYILGDNGAHINSGOSGVAAKTSYTFELVKSMIETSSKNGDLMRELREARYIFNVKG		2222
QY	52	GTTTLTKKIEVYVEWALDATAKYE-FRVVELDPSAKIEVYTYDNKKKTEKTSFPTTEKG	110	
Db	223	ESLFLDRIIS--KEWTSEREKDEMRVLGIEPKPFENVAEY-----APGREK 269		

Query Match 10.9%; Score 78; DB 2; Length 350;
Best Local Similarity 32.8%; Pred. NO. 13;
Matches 22; Conservative 14; Mismatches 23; Indels 8; Gaps 4;

QY 59 KLEYVWEALDATAKFEFRVVVELDPSAKIEVTYYIDKNKKKEETKSFPITEKGfv---vPD 115
||| || | || : | | : | | : | | : | : |
Db 138 KISKVK--LLD--LYKDVB-TELSKGRSEVVHYAKERMKEIVRNyFVEAKWFIEGYMPp 192
: || : |
QY 116 LSEHIKN 122
:||: |
Db 193 VSEYLNN 199

RESULT 10
ITBPT4
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) medium chain - phase T4
N:Alternate names: DNA topoisomerase II; DNA-gyrase
C:Species: Phase T4
C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 05-Jun-1998
C:Accession: B24705; S01872
R:Huang, W.M.
Nucleic Acids Res. 14, 7379-7390, 1986
A>Title: The 52-protein subunit of T4 DNA topoisomerase is homologous to the gyra-protein
A:Reference number: A24705; MUID:87016377
A:Accession: B24705
A:Molecule type: DNA
A:Residues: 1-441 <HUA>
R:Chapman, D.; Morad, I.; Kaufmann, G.; Gait, M.J.; Jorissen, L.; Snyder, L.
J. Mol. Biol. 199, 373-377, 1986
A>Title: Nucleotide and deduced amino acid sequence of stp: the bacteriophage T4 anticomplex
A:Reference number: S01711; MUID:88172481
A:Accession: S01872
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-46 <CHA>
C:Genetics:
A:Gene: 52
A:Map position: 162-164 kb
C:Complex: this is the middle-sized of the three subunits of T4 DNA topoisomerase
C:Superfamily: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain; phase T4 DNA
C:Keywords: DNA binding; DNA replication; isomerase
E:1-225/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <TOP>

Query Match 10.8%; Score 77.5; DB 1; Length 441;
Best Local Similarity 25.5%; Pred. No. 20;
Matches 36; Conservative 21; Mismatches 43; Indels 41; Gaps 8;

QY 16 SYFPEPTGPLYMVNV-VTGVDKSGNELSPHHVVEFFIK-----PGTTLTKEKIEYIYEVAL 68
::: | : :::: |: : | | : | | : | : | : |
Db 147 AFYLPILPTVLLNGSVGIATGYATPYLPHSVSSVKKAVALQAOLCKKVTRPKVE----- 199
::: | : :::: |: : | | : | | : | : | : |
QY 69 DATAYAKEFR--VWELDSPSAKIEVTY-----YDKNKKEETKSF-PITEKGF 111
: || | | | : | : | : | : | : | : | : |
Db 200 ----FPERGEVVIDQGEIRGTYSRTQMHITEIPYKYDRETYVSKILOPLENKGF 255
: | | | | : | : | : | : | : | : | : |
QY 112 VVPD--LSEHKNPGNLTIK 130
: | | | : | : | : | : | : | : | : |
Db 256 ITWDADACGEH----GFGFKVK 272

RESULT 11
T08174
sesquiterpene cyclase (EC 2.5.1.-) - pepper
C:Species: Capsicum annuum (pepper)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08174
R:Back, K.; Shin, D.H.; He, S.
Plant Cell Physiol. 39, 899-904, 1998
A>Title: Cloning and bacterial expression of sesquiterpene cyclase, a key branch point e
A:Reference number: Z16395; MUID:99033462

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:41:34 ; Search time 11.66 Seconds
(without alignments)
427.651 Million cell updates/sec

Title: US-09-601-490-1
Perfect score: 715
Sequence: 1 SSSFDKGYKGGDASIFEP.....SEHIKNPGFNLTIVKVIKK 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	99.4	163	SAK_STAAU	P00802 staphylococ
2	695	97.2	163	SAK_BPP42	P15240 bacterioph
3	84.5	11.8	172	YB13_FOWPM	P14368 fowlpox vir
4	80.5	11.3	3097	CADN_DROME	O15943 drosophila
5	78.5	11.0	324	YF02_METJA	Q58897 methanococ
6	78.5	11.0	719	IF39_TOBAC	P56821 nicotiana t
7	77.5	10.8	442	TOP5_BPT4	P07065 bacterioph
8	77	10.8	608	PLRL_MOUSE	Q08501 mus musculu
9	76.5	10.7	506	VL1_BPV4	P08341 bovine papi
10	75.5	10.6	327	LXBI_PHOLU	P19840 photorhabd
11	75	10.5	576	NAE2_THEMA	Q9x0y0 thermotoga
12	74.5	10.4	2511	FAS_CHICK	P12276 gallus gall
13	74	10.3	298	MOAA_METJA	Q58234 methanococ
14	74	10.3	610	PLRL_RAT	P05710 rattus norv
15	73.5	10.3	430	SERC_ARATH	Q96255 arabidopsis
16	73	10.2	231	CTRA_CAUCR	Q45994 caulobacter
17	73	10.2	237	TRMD_BUCAI	P57476 buchnera ap
18	73	10.2	263	YPUB_ECOLI	P76612 escherichia
19	73	10.2	2505	FAS_RAT	P12785 rattus norv
20	73	10.2	4969	RYNC_RABIT	P30957 oryctolagus
21	72.5	10.1	374	YEAU_ECOLI	P76253 escherichia
22	72.5	10.1	430	SURA_BUCAI	P57240 buchnera ap
23	72.5	10.1	935	IF38_MEDTR	Q9xhml medicago tr
24	72.5	10.1	1043	SYI_CHLPN	Q92972 chlamydia p
25	72	10.1	429	HISX_METJA	Q58851 methanococ
26	72	10.1	695	APP2_MOUSE	Q06335 mus musculu
27	72	10.1	978	KFMS_RAT	Q00495 rattus norv
28	72	10.1	1102	YE20_METJA	Q58815 methanococ
29	72	10.1	2663	CENE_HUMAN	Q02224 homo sapien
30	71.5	10.0	553	YF61_METJA	Q58956 methanococ
31	71.5	10.0	560	POTA_MYCPN	P75059 mycoplasma
32	71.5	10.0	667	Y366_MYCGE	P47606 mycoplasma
33	71.5	10.0	686	FREL_YEAST	P32791 saccharomyc

ALIGNMENTS

RESULT 1

ID	SAK_STAAU	STANDARD;	PRT;	163 AA.
AC	P00802;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III).			
GN	SAK.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84069795; PubMed=6359061;			
RA	Sako T., Tsuchida N.;			
RT	"Nucleotide sequence of the staphylokinase gene from Staphylococcus aureus.";			
RL	Nucleic Acids Res. 11:7679-7693(1983).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 43-163.			
RX	MEDLINE=97290447; PubMed=9145104;			
RA	Rabljns A., de Bondt H.L., de Ranter C.;			
RT	"Three-dimensional structure of staphylokinase, a plasminogen activator with therapeutic potential.";			
RL	Nat. Struct. Biol. 4:357-360(1997).			
RN	[3]			
RP	STRUCTURE BY NMR OF 28-163.			
RX	MEDLINE=98367505; PubMed=9692953;			
RA	Ohlenschlaeger O., Ramachandran R., Guehrs K.H., Schlott B., Brown L.R.;			
RT	"Nuclear magnetic resonance solution structure of the plasminogen-activator protein staphylokinase.";			
RL	Biochemistry 37:10635-10642(1998).			
CC	-!- FUNCTION: THIS EXTRACELLULAR PROTEIN IS ONE OF THE PLASMINOGEN ACTIVATORS THAT CONVERTS PLASMINOGEN INTO PLASMIN; IT REQUIRES CALCIUM ION FOR STABILIZATION.			
CC	-----			
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CC	-----			
CC	EMBL; X00127; CAA24957.1; -.			
DR	PIR; A00995; PRSAK.			
DR	PDB; 2SAK; 25-FEB-98.			
DR	PDB; 1SSN; 02-DEC-98.			
KW	Hydrolase; Calcium; 27			
FT	SIGNAL 1			
FT	CHAIN 28 163			
SQ	SEQUENCE 163 AA; 18490 MW; E56D9FF50AEDE141 CRC64;			

P14788 synchococc
Q27367 drosophila
P26404 salmonella
P12048 b bifunctio
Q54873 streptococ
P09581 mus musculu
P41885 caenorhabdi
P39077 saccharomyc
Q9hnc4 pyrococcus
Q04399 saccharomyc
P75432 mycoplasma
Q57703 methanococc

Query Match	97.2%	Score 695;	DB 1;	Length 163;
Best Local Similarity	97.8%;	Pred. No. 2.6e-57;		
Matches 133; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	SSSFDKGYKKDDASYEPTGPIYLVNVTGVDSKGNELLSPHYVEFPKPGTTLTKKI	60	
Db	28	SSSFDKGYKKDDASYEPTGPIYLVNVTGVDSKGNELLSPHYVEFPKPGTTLTKKI	87	
QY	61	EYYVEWALDATAYKEFRVVELDPSAKTEVTVYDKNKKKEETKSFPTTEGFVVPDLSHI	120	
Db	88	EYYVEWALDATAYKEFRVVELDPSAKTEVTVYDKNKKKEETKSFPTTEGFVVPDLSHI	147	

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QY 121 KNPGFNLTIKVWIEKK 136
      |||
Db 148 KNPGFNLTIKVWIEKK 163

RESULT 3
YB13_FOWPM STANDARD; PRT; 172 AA.
AC P14368;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FLOWPOXITICAL BAMHI-ORF13 PROTEIN (FRAGMENT).
OS FLOWPOX VIRUS (isolate HP-438[Munich]).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; ACNIPoxvirus.
OX NCBI_TaxID=10263;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88229622; PubMed=2836548;
RA Tomley F., Blinn M., Campbell J., Boursnell M.;
RT "Sequence analysis of an ll.2 kilobase, near-terminal, BamHI fragment of fowlpox virus.";
RL J. Gen. Virol. 69:1025-1040(1988).
CC -!- SIMILARITY: CONTAINS AT LEAST 5 ANK REPEATS.
-----
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-----
DR D00295; BAA00209.1; -.
PIR: D30087; WMVZTH.
DR InterPro: IPR002110; ANK.
PFam: PF00023; ank; 4.
SMART: SMART_000248; ANK; 3.
DR PROSITE; PS00088; ANK_REPEAT; 3.
DR PROSITE; PS02097; ANK_REP_REGION; 1.
KW Hypothetical protein; Early protein; Repeat; ANK repeat.
FT NON_TER 1 1
FT REPEAT 7 36 ANK 1.
FT REPEAT 39 68 ANK 2.
FT REPEAT 73 105 ANK 3.
FT REPEAT 110 138 ANK 4.
FT REPEAT 143 172 ANK 5.
SQ SEQUENCE 172 AA; 19560 MW; 1929D02DC8C86457 CRC64;

Query Match 11.8%; Score 84.5; DB 1; Length 172;
Best Local Similarity 25.2%; Pred.No.0.48;
Matches 31; Conservative 19; Mismatches 36; Indels 37; Gaps 5;

QY 43 HYVEFFPKPTTLTKEXI-EYYVEWALDATA-----YKEFRV---VEL 81
||| ||| :|: |:: |:| :|: |
Db 38 HYLKLPHTIAANRSTESVIKLLIEYGADINSEGDANGKYPIHYAMKVDPFLRKIIKVL 97

QY 82 DPSAKLEVTVYDNKKKEETKSPITEKGFWVPDLSEHKNPQNL-----ITKVV 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 98 DHGA-----DINKOSVLTNTSPLYTRFITDDLDYIISRGANINIKEWVEYITRII 150

QY 133 IEK 135
| |
Db 151 LER 153

RESULT 4
CADN_DROME STANDARD; PRT; 3097 AA.
ID CADN_DROME
AC Q15943; Q9VJB7;
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FT DISULFID 2351 2366 POTENTIAL.
FT DISULFID 2368 2377 POTENTIAL.
FT DISULFID 2592 2607 POTENTIAL.
FT DISULFID 2601 2616 POTENTIAL.
FT DISULFID 2618 2627 POTENTIAL.
FT DISULFID 2869 2880 POTENTIAL.
FT DISULFID 2874 2891 POTENTIAL.
FT DISULFID 2893 2902 POTENTIAL.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 930 930 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1266 1266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 1425 1425 E -> K (IN ALLELE CADN-M12; MUSCLE DEFECTS).
FT CONFLICT 1342 1342 P -> A (IN REF. 1).
FT CONFLICT 2786 2786 S -> T (IN REF. 1).
SQ SEQUENCE 3097 AA; 347201 MW; 082242F28D9B5CC3 CRC64;

Query Match 11.3%; Score 80.5; DB 1; Length 3097;
Best Local Similarity 27.6%; Pred. No. 37;
Matches 45; Conservative 16; Mismatches 55; Indels 47; Gaps 9;

QY 13 DDASYFEPTGPLYMNVNTGVDKGNELSP-----HYVEFPKPGTTLTKEK----- 59
Df 731 EDGGFSTVSDLTIRTVNDNAPKFPDLYQAHNVDEDIPLGTSLRVKAMDSDSGSN 789
QY 60 --IEYVV---EWALDA-----TAYKEFRVVELD-----PSAKIEVTYDK 94
Df 790 AEIYVSDHDFAVDSNGIIVNNKQLDADNNAYEYFIVTAKDKGEPKSGVATRVYTK 849
QY 95 NKKKEETKSPITKGFVVDLSEHIKNPGFN-LITKVIIEK 136
Df 850 NKDEE---PKFSQQVYTPNVDE---NAGPNTLVTTVWASDK 885

RESULT 5
YF02_METJA STANDARD; PRT; 324 AA.
AC Q58897;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1502.
GN MJ1502.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Cocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE ATSA / ELAC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y11996; CAAY2721.1;
CC InterPro; IPR000504; RRM.
CC Pfam; PF00076; rrm; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 60 147 RNA-BINDING (RRM).
SQ SEQUENCE 719 AA; 82524 MW; BBFA223B7DA52BB2 CRC64;
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67591; AAB99515.1;
CC TIGR; MJ1502;
CC InterPro; IPR001279; Beta_lactam_met.
CC Pfam; PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 324 AA; 36893 MW; A3DF62E3BAAEEFA4 CRC64;

Query Match 11.0%; Score 78.5; DB 1; Length 324;
Best Local Similarity 24.2%; Pred. No. 3.7;
Matches 39; Conservative 18; Mismatches 57; Indels 47; Gaps 7;

QY 7 GYKKGKGDASYFEPTGPLYMNVNTGVDKGNEL-LSPHYVEFPKPGTTLTKEKIEYVE 65
Df 87 GFGREKELKIFGEGTKEIE-----NSLKLGHYIEFPKYEIYTKPEITTYKE 138
QY 66 WALDATAY-----KEFRVVELD--PSAKIEVTYDKNKK----- 97
Df 139 ENVEIIAYPTEHGIPSYAYIFKEIKKPRLDIERAKKLGVKIGPDLKLNKNGEAVKNIYE 198
QY 98 --KEE-----TKSPITEKGFVVP--DLSEHIKNPGFNLI 128
Df 199 IIRPEVLLPPKKGFCLAYSGDITPLEDFGKYLKELGCDVL 239

RESULT 6
IF39_TOBAC STANDARD; PRT; 719 AA.
ID IF39_TOBAC
AC P56821;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF-3 ETA) (EIF3 P110).
DE P110.
GN PRT1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, BRIGHT YELLOW 2;
RA Shen W.H., Gigot C.;
RT "Characterization of prt1, a gene encoding for one of the subunits of
RL the translation initiation factor 3 (eif3), from Nicotiana tabacum."
CC Plant Sci. 143:45-54(1999).
CC -!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MRNA.
CC -!- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS (BY
CC SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -----
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CC -----
CC EMBL; Y11996; CAAY2721.1;
CC InterPro; IPR000504; RRM.
CC Pfam; PF00076; rrm; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 60 147 RNA-BINDING (RRM).
SQ SEQUENCE 719 AA; 82524 MW; BBFA223B7DA52BB2 CRC64;
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KW Isomerase; Topoisomerase; DNA-binding.
FT ACT_SITE 117 117 5'-ENDS OF THE DNA VIA A PHOSPHO-TYROSYL
SQ SEQUENCE 442 AA; 50493 MW; 519E60AEE6F75AF7 CRC64;

Query Match 10.8%; Score 77.5; DB 1; Length 442;
Best Local Similarity 25.5%; Pred. No. 6.7; Indels 41; Caps 8;
Matches 36; Conservative 21; Mismatches 43;

QY 4 FDGKVKGGDASYF-----EPTGPLYMNVNVTGVDKGN-----ELLSPH 43
DB 543 FDVELETWASAHFWATDVEWDOPTGRYVATSVTSHENGNGINWSFGKLLYRLKDH 602

QY 44 YVEF---PIKPGTTLTKKIEKYVEWALDATAY-KEFRVVDPSAKIEVYVYDKNKK-K 98
DB 603 FFQYLWRP-RPPSFLSKREE---ETAKNLKRYSKKYAEADQDVSLSLQSDREKRKKLK 658

QY 99 EETKSF 104
DB 659 EEWEAW 664

RESULT 7
TOP5_BPT4 STANDARD; PRT; 442 AA.
AC P07065;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE DNA TOPOISOMERASE MEDIUM SUBUNIT (EC 5.99.1.3) (PROTEIN GP52).
GN 52.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OC T4-like phages.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87016377; PubMed=3020513;
RA Huang W.M.;
RT "The 52-protein subunit of T4 DNA topoisomerase is homologous to the
RL gyra-protein of gyrase."
RL Nucleic Acids Res. 14:7379-7390(1986).
RN [2]
RP REVISIONS.
RA Huang W.M.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-46 FROM N.A.
RX MEDLINE=88172481; PubMed=3280805;
RA Chapman D., Morad I., Kaufmann G., Gait M.J., Jorissen L., Snyder L.;
RT "Nucleotide and deduced amino acid sequence of stp: the bacteriophage
RL T4 anticodon nuclease gene."
RL J. Mol. Biol. 199:373-377(1988).
CC -!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. T4 TOPOISOMERASE
CC MAKES DOUBLE-STRAND BREAKS.
CC -!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
CC OF DOUBLE-STRANDED DNA.
CC -!- SUBUNIT: THIS IS ONE OF THE 3 SUBUNITS OF T4-DNA TOPOISOMERASE.
CC -!- SIMILARITY: TO THE PROKARYOTIC GYRASE SUBUNIT A AND TO EUKARYOTIC
CC TOPOISOMERASE II.
CC -----
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CC -----
CC EMBL: X04376; CAA27959.1; ..
CC PIR: B24705; ITBPT4.
CC DR PIR: S01872; S01872.
CC DR InterPro: IPR002205; DNA_topoisomIV.
CC DR Pfam: PF00521; DNA_topoisomIV; 1.
CC DR SMART: SM00434; TOP4c; 1.
CC -----

KW Isomerase; Topoisomerase; DNA-binding.
FT ACT_SITE 117 117 5'-ENDS OF THE DNA VIA A PHOSPHO-TYROSYL
SQ SEQUENCE 442 AA; 50493 MW; 519E60AEE6F75AF7 CRC64;

Query Match 10.8%; Score 77.5; DB 1; Length 442;
Best Local Similarity 25.5%; Pred. No. 6.7; Indels 41; Caps 8;
Matches 36; Conservative 21; Mismatches 43;

QY 16 SYFEPGPLYMNVN-VTGVDSKGNELLSPHYVEFPK-----FCTTLTKKIEKYVEWAL 68
DB 148 AFVLPITPTVLLNGVSGIATGYATILPHSVSSVKRAVLQALQGVKVKPKVE----- 200

QY 69 DATAYKEFR--VVELDPSAKIEVY-----YDNKKKEETKSF-PIEKGK 111
DB 201 ----FPEFRGEVVEIDQVEIRGTYKTSRTQMHTEIPYKYDRETYVSVKILDPLENKGF 256

QY 112 VVPD--LSEHIKNPGENLITK 130
DB 257 ITWDDACGEH----GFGFKVK 273

RESULT 8
PRLR_MOUSE STANDARD; PRT; 608 AA.
ID PRLR_MOUSE
AC Q08501; Q62099; P15213; P15212;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=C3H; TISSUE=Mammary gland;
RX MEDLINE=94085788; PubMed=8262385;
RA Moore R.C., Oka T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RL long-form prolactin receptor."
RL Gene 134:263-265(1993).
RN [2]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=SWISS WEBSTER; TISSUE=Liver;
RX MEDLINE=93307149; PubMed=8319571;
RA Clarke D.L., Linzer D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RL mouse ovary."
RL Endocrinology 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA Sasaki M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=BALB/C; TISSUE=Mammary gland;
RA Edery M., Pezet A., Nandi S., Kelly P.A.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RC STRAIN=SWISS WEBSTER; TISSUE=Liver;
RX MEDLINE=89261824; PubMed=2725531;
RA Davis J.A., Linzer D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse
RL liver."
RL Mol. Endocrinol. 3:674-680(1989).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; PRL-R1, PRL-R2 AND PRL-R3 (SHOWN
```

CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; L13593; AAC37641.1; -;
DR EMBL; L14811; AAA02686.1; -;
DR EMBL; D10214; BAA01066.1; -;
DR EMBL; X73372; AAA51789.1; -;
DR EMBL; M22959; AAA39977.1; -;
DR EMBL; M22958; AAA39976.1; -;
DR PIR; J0671; J0671.
DR HSP; P16471; IBP3.
DR MGD; MGI:97763; PrIr.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR001777; FN III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 608 PROLACTIN RECEPTOR.
FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
FT TRANSEM 230 253 BY SIMILARITY.
FT DOMAIN 254 608 CYTOPLASMIC (BY SIMILARITY).
FT DOMAIN 20 117 FIBRONECTIN TYPE-III 1.
FT DOMAIN 119 222 FIBRONECTIN TYPE-III 2.
FT DISULFID 31 41 BY SIMILARITY.
FT DISULFID 70 81 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 281 292 KGKSEELLSALG -> VHNKEQLENVYV (IN ISOFORM PRL-R2).
FT VARSPLIC 293 608 MISSING (IN ISOFORM PRL-R2).
FT VARSPLIC 281 303 KGKSEELLSALGDFPPTSDCE -> LMCSILQLSLVKI
FT PTFEFLCDL (IN ISOFORM PRL-R1).
FT VARSPLIC 304 608 MISSING (IN ISOFORM PRL-R1).
FT CONFLICT 558 558 L -> F (IN REF. 2).
SQ SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;

Query Match 10.8%; Score 77; DB 1; Length 608;
Best Local Similarity 23.9%; Pred. No. 11;
Matches 34; Conservative 17; Mismatches 43; Indels 48; Gaps 7;

QY 4 FDGKGYKGGDASY-----PEPTGPY--LMVNTGVDSKGNELLSP-HYVEFP---I 49
DB 274 FTHLLKSGKSEELLSALGQDFPPTSDCEDLLVEFLVEDDNERLMPHSKEYPQGV 333
QY 50 KPGTTLTKKIEYVVEWALDATAYKEPRVVELDPDSAKIEVYTDK----NKKKEETKSPF 105
DB 334 KP-----THLPDSDSGHGSYDSSLSEKCEEPQAYP 366

QY 106 ITEKGFVVPDLSHKNPGLN 127
ID VLI_BPV4 STANDARD; PRT; 506 AA.
AC P08341;
DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MAJOR CAPSID PROTEIN L1.
GN L1.
OS Bovine papillomavirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87282264; PubMed=3039043;
RA Patel K.R., Smith K.T., Campo M.S.;
RT "The nucleotide sequence and genome organization of bovine
RL papillomavirus type 4.";
RL J. Gen. Virol. 68:2117-2128(1987).
CC -----
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CC -----
DR EMBL; X05817; -; NOT_ANNOTATED_CDS.
DR EMBL; D00146; BAA00101.1; -;
DR PIR; B26214; PIWLB4.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_CAPSID_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 506 AA; 57902 MW; FLC5DFDB54FA681E CRC64;

Query Match 10.7%; Score 76.5; DB 1; Length 506;
Best Local Similarity 28.7%; Pred. No. 9.7;
Matches 29; Conservative 19; Mismatches 36; Indels 17; Gaps 7;

QY 29 TVGVDG-KG-NELLSPHYVEFPKPGTTLTKKIEYVYV----EWALDATAYKEFRVVELD 82
DB 331 VTAVDSTRGTFNSVHTDPEVKPQETATATKFKHYLRHVEW--DLSLMQLCIVNLT 388
QY 83 PSKIEVYTDKNNKKEETKSPFITEKGFVVP--DLSEHIK 121
DB 389 P-----ESIAYLHNWESIIENWNL---GFTQPPNDIEDHYR 422

RESULT 10
LXBL_PHOLU STANDARD; PRT; 327 AA.
AC P19840;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE ALKANAL MONOOXYGENASE BETA CHAIN (EC 1.14.14.3) (BACTERIAL LUCIFERASE
DE BETA CHAIN).
GN LUXB.
OS Photobacterium luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Photobacterium.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29999;
RX MEDLINE=90375532; PubMed=2204626;
RA Szitner R., Weighen E.;
RT "Nucleotide sequence, expression, and properties of luciferase coded
RL by lux genes from a terrestrial bacterial bacterium.";
RN J. Biol. Chem. 265:16581-16587(1990).
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29999;

DE FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39;
DE EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14].
GN EASN OR FAS.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-11.
RC STRAIN=WHITE LEGHORN; TISSUE=Liver;
RX MEDLINE=95031085; PubMed=7944406;
RA Huang W.-Y., Chirala S.S., Wakil S.J.;
RT "Amino-terminal blocking group and sequence of the animal fatty acid
RT synthase.";
RL Arch. Biochem. Biophys. 314:45-49(1994).
RN [2]
RP SEQUENCE OF 75-1775 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89282777; PubMed=2734291;
RA Holzer K.P., Liu W., Hammes G.G.;
RT "Molecular cloning and sequencing of chicken liver fatty acid
RT synthase cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4387-4391(1989).
RN [3]
RP SEQUENCE OF 1568-2512 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89139426; PubMed=2917973;
RA Chirala S.S., Kasturi R., Pazirandeh M., Stelow D.T., Huang W.-Y.,
RA Wakil S.J.;
RT "A novel cDNA extension procedure. Isolation of chicken fatty acid
RT synthase cDNA clones.";
RL J. Biol. Chem. 264:3750-3757(1989).
RN [4]
RP SEQUENCE OF 1752-2512 FROM N.A.
RX MEDLINE=88320436; PubMed=2842766;
RA Yuan Z., Liu W., Hammes G.G.;
RT "Molecular cloning and sequencing of DNA complementary to chicken
RT liver fatty acid synthase mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:6328-6331(1988).
RN [5]
RP SEQUENCE OF 2202-2512 FROM N.A.
RX MEDLINE=89088152; PubMed=3207710;
RA Kasturi R., Chirala S.S., Pazirandeh M., Wakil S.J.;
RT "Characterization of a genomic and cDNA clone coding for the
RT thioesterase domain and 3' noncoding region of the chicken liver
RT fatty acid synthase gene.";
RL Biochemistry 27:7778-7785(1988).
RN [6]
RP SEQUENCE OF 2121-2209.
RX MEDLINE=89192401; PubMed=2648999;
RA Huang W.-Y., Stoops J.K., Wakil S.J.;
RT "Complete amino acid sequence of chicken liver acyl carrier protein
RT derived from the fatty acid synthase.";
RL Arch. Biochem. Biophys. 270:92-98(1989).
RN [7]
RP SEQUENCE OF 2209-2508.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=89088151; PubMed=3207709;
RA Yang C.-Y., Huang W.-Y., Chirala S.S., Wakil S.J.;
RT "Complete amino acid sequence of the thioesterase domain of chicken
RT liver fatty acid synthase.";
RL Biochemistry 27:7773-7777(1988).
RN [8]
RP SEQUENCE OF 667-674 AND 1698-1709.
RX MEDLINE=89323081; PubMed=2751995;
RA Chang S.I., Hammes G.G.;
RT "Amino acid sequences of pyridoxal 5'-phosphate binding sites and
RT fluorescence resonance energy transfer in chicken liver fatty acid
RT synthase.";
RL Biochemistry 28:3781-3788(1989).
CC CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES AND AN

ACYL CARRIER PROTEIN.
-1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).
-1- CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA
+ ACETYL-[ACYL-CARRIER PROTEIN].
-1- CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN] = COA
+ MALONYL-[ACYL-CARRIER PROTEIN].
-1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + MALONYL-[ACYL-
CARRIER PROTEIN] = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + CO(2) +
[ACYL-CARRIER PROTEIN].
-1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
-1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
= 2-HEXADECENOYL-[ACYL-CARRIER PROTEIN] + H(2)O.
-1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NADP(+) = 2,3-
DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADPH.
-1- CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] + H(2)O =
ACYL-CARRIER PROTEIN + OLEATE.
-1- SUBUNIT: HOMODIMER, WHICH IS ARRANGED IN A HEAD TO TAIL FASHION.
-1- CAUTION: REF.3 AND REF.5 SEQUENCES DIFFER FROM THAT SHOWN FROM
POSITION 2351 ONWARDS DUE TO A FRAMESHIFT.

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EMBL: J04485; AAB46389.1; -
DR EMBL: J03860; AAA48767.1; -
DR EMBL: J02839; AAC82106.1; ALT_SEQ.
DR PIR: A33918; XYCHEFA.
DR PIR: A32015; A32015.
DR HSP: P02901; IACP.
DR InterPro: IPR001227; Acyltransf_domain.
DR InterPro: IPR002085; Adh_zinc.
DR InterPro: IPR000794; Ketoacyl-synt.
DR InterPro: IPR003880; Phosphopant_attach.
DR InterPro: IPR001031; Thioesterase.
DR Pfam: PF00698; Acyl_transf; 1.
DR Pfam: PF00107; adh_zinc; 1.
DR Pfam: PF00109; ketoacyl-synt; 1.
DR Pfam: PF00550; pp-binding; 1.
DR Pfam: PF00975; Thioesterase; 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS00075; ACP_DOMAIN; 1.
KW Fatty acid biosynthesis; Multifunctional enzyme; Phosphopantetheine;
KW Transferase; Hydrolase; Oxidoreductase; Lyase; NADP; Acetylation;
FT Alternative splicing.
FT INIT_MET 0 0
FT DOMAIN 1 7411 BETA-KETOACYL SYNTHASE.
FT DOMAIN 427 815 ACYL AND MALONYL TRANSFERASES.
FT DOMAIN 1638 1866 ENOYL REDUCTASE.
FT DOMAIN 1867 2119 BETA-KETOACYL REDUCTASE.
FT DOMAIN 2124 2180 ACYL CARRIER (ACP).
FT DOMAIN 2209 2511 THIOESTERASE.
FT MOD_RES 1 1 ACETYLATION.
FT ACT_SITE 160 160 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT ACT_SITE 579 579 ACYL/MALONYL TRANSFERASES (BY
FT ACT_SITE 877 877 SIMILARITY).
FT ACT_SITE 877 877 BETA-HYDROXYACYL DEHYDRATASE (BY
FT NP_BIND 1674 1691 NADP (ER).
FT BINDING 1707 1707 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT NP_BIND 1888 1903 NADP (KR).
FT BINDING 2157 2157 PHOSPHOPANTETHEINE (BY SIMILARITY).
FT ACT_SITE 2308 2308 THIOESTERASE (BY SIMILARITY).
FT ACT_SITE 2348 2481 THIOESTERASE (BY SIMILARITY).
FT VARSPIC 2348 2348 T -> TQCFSESLF (IN ISOFORM 1).
FT CONFLICT 77 78 QL -> PV (IN REF. 2).

```
FT CONFLICT 116 116 L -> A (IN REF. 2).
FT CONFLICT 675 675 R -> S (IN REF. 2).
FT CONFLICT 1169 1169 K -> N (IN REF. 2).
FT CONFLICT 1178 1178 A -> T (IN REF. 2).
FT CONFLICT 1191 1191 R -> H (IN REF. 2).
FT CONFLICT 1198 1198 P -> L (IN REF. 2).
FT CONFLICT 1286 1287 DN -> ND (IN REF. 2).
FT CONFLICT 1372 1372 K -> E (IN REF. 2).
FT CONFLICT 1533 1533 W -> Y (IN REF. 2).
FT CONFLICT 1577 1577 W -> R (IN REF. 2).
FT CONFLICT 1685 1696 QAAIAIALSMGCG -> ASSHCHRLHGLA
      (IN REF. 2; AAA48767).
FT CONFLICT 1732 1732 Q -> E (IN REF. 2).
FT CONFLICT 1745 1745 S -> N (IN REF. 2).
FT CONFLICT 2511 2511 AA; 274648 MW; 622039DNC8315D3F CRC64;
SQ SEQUENCE 2511 AA; 274648 MW; 622039DNC8315D3F CRC64;

Query Match 10.4%; Score 74.5; DB 1; Length 2511;
Best Local Similarity 25.5%; Pred. No. 1e+02;
Matches 26; Conservative 13; Mismatches 24; Indels 39; Gaps 5;

QY 27 VNVGTGDSKGNELSPHYVEFPKPGTTTKKIEYVVEWALDATAKFRVVELDPSAK 86
DB 801 IHLTGINVLGNLFPB--VEYVPVCTPL-----ISPYIKW-----DHSQD 839

QY 87 IEVYYDNKKKEETKSPITEKGF-----VVPDLSEH 119
DB 840 WDV-----PKAEDFSGSKGSASAVYINIDVSPDSPDH 872

RESULT 13
MOAA_METJA
ID MOAA_METJA STANDARD; PRT; 298 AA.
AC Q58234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE MOLYBDOPTERIN COFACTOR SYNTHESIS PROTEIN A.
GN MOAA OR MJ0824.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF MOLYBDOPTERIN PRECURSOR
CC 2- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS (BY SIMILARITY).
CC -1- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MOAA / NIFB / PQOE FAMILY.
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CC -----
DR EMBL; U67526; AAB98823.1;
DR TIGR; MJ0824;

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DR InterPro; IPR000385; MoAA_NifB_PqqE.
DR Pfam; PF01444; MoAA_NifB_PqqE; 1.
DR PROSITE; PS01305; MOAA_NIFB_PQOE; 1.
KW Molybdenum cofactor biosynthesis; Iron-sulfur; Complete proteome.
FT METAL 20 20 IRON-SULFUR (POTENTIAL).
FT METAL 24 24 IRON-SULFUR (POTENTIAL).
FT METAL 27 27 IRON-SULFUR (POTENTIAL).
SQ SEQUENCE 298 AA; 34652 MW; EA92B9A0A75BFD55 CRC64;

Query Match 10.3%; Score 74; DB 1; Length 298;
Best Local Similarity 21.4%; Pred. No. 8.7;
Matches 21; Conservative 19; Mismatches 42; Indels 16; Gaps 1;

QY 31 GVDKGNELSPHYVEFPKPGTTTKKIEYVVEWALDATAKFRVVELDPSAKIEVT 90
DB 31 GHDSNNDRYMTPEEIGIIARTKSTKFGVKKI-----KISGGEFLLRKQVC 74

QY 91 YVDKNNKKEETKSPITEKGFVVPDLSEHIKNPGENLI 128
DB 75 EIIENIKDKRIDISLTNGILLNLAELKLDAGLNRV 112

RESULT 14
PRLR_RAT
ID PRLR_RAT STANDARD; PRT; 610 AA.
AC P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91155946; PubMed=2293022;
RA Shiota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,
RA Edery M., Djiane J., Kelly P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and
RT liver."
RL Mol. Endocrinol. 4:1136-1143(1990).
RN [2]
RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;
RX MEDLINE=90241201; PubMed=2159291;
RA Zhang R., Buczko E., Tsai-Morris C.H., Hu Z.Z., Dufau M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen
RT receptor cDNA species."
RL Biochem. Biophys. Res. Commun. 168:415-422(1990).
RN [3]
RP SEQUENCE OF 281-610 FROM N.A.
RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RC TISSUE=Liver;
RX MEDLINE=88165059; PubMed=2832068;
RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edery M.,
RA Shiota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of
RT the growth hormone/prolactin receptor gene family."
RL Cell 53:69-77(1988).
RN [5]
RP SEQUENCE FROM N.A. (FORM NB2).
RC TISSUE=Lymphoma;
RX MEDLINE=92041834; PubMed=1718958;
RA Ali S., Pelligrini I., Kelly P.A.;
RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
RT of prolactin receptor."
RL J. Biol. Chem. 266:20110-20117(1991).
```

[6]
 RN SEQUENCE FROM N.A. (FORM NB2).
 RX MEDLINE=95014432; PubMed=7929319;
 RA O'Neal K.D., Yu-Lee L.Y.;
 RT "Differential signal transduction of the short, Nb2, and long
 RT prolactin receptors. Activation of interferon regulatory factor-1 and
 RT cell proliferation.";
 RL J. Biol. Chem. 269:26076-26082(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING OF THE PRLR GENE.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC
 CC EMBL; M57668; AAA41938.1; -
 CC EMBL; M34083; AAA79273.1; -
 CC EMBL; L48060; AAA79274.1; -
 CC EMBL; U34730; AAA92053.1; -
 CC EMBL; M19304; AAA41937.1; -
 CC EMBL; M74152; AAA41946.1; -
 CC EMBL; U07567; AAA61784.1; -
 CC PIR; A29884; A29884.
 CC HSSP; P16471; IBP3.
 CC InterPro; IPR002996; CR1A.
 CC InterPro; IPR001777; FN_III.
 CC InterPro; IPR003528; Hematopo_rceptor_L_F1.
 CC Pfam; PF00041; fn3; 2.
 CC SMART; SM00060; FN3; 1.
 CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 CC Alternative splicing.
 CC SIGNAL 1 19
 CC CHAIN 20 610
 CC DOMAIN 20 229
 CC TRANSMEM 230 253
 CC DOMAIN 254 610
 CC DOMAIN 20 117
 CC DOMAIN 119 222
 CC DISULFID 31 41
 CC DISULFID 70 81
 CC CARBOHYD 54 54
 CC CARBOHYD 99 99
 CC CARBOHYD 127 127
 CC VARSPLIC 131 150
 CC VARSPLIC 151 610
 CC VARSPLIC 281 310
 CC VARSPLIC 311 610
 CC VARSPLIC 342 539
 CC CONFLICT 236 236
 CC CONFLICT 345 345
 CC CONFLICT 465 465
 CC CONFLICT 466 466
 CC CONFLICT 469 469
 CC CONFLICT 541 541
 CC CONFLICT 555 555
 CC SEQUENCE 610 AA; 68599 MW; 83D04D832861295D CRC64;
 Query Match 10.3%; Score 74; DB 1; Length 610;
 Best Local Similarity 23.9%; Pred. No. 21;

Matches 34; Conservative 17; Mismatches 43; Indels 48; Gaps 7;
 QY 4 FDKGKYKGDASY-----FEPTGPY--LMVNTGVDSKGNELSP--HYVEFP---I 49
 Db 274 FDTHLEKKGKSEILLSALGQCDPPTSDCEDLLVEFLVEDNEDRLMPHSKEYPCQGV 333
 QY 50 KPGTTLTKKIEYVWALDATALYKFRVVELDPSAKIEVYYDK-----NKKKEETKSPF 105
 Db 334 KP-----THLDPDSDSGHSGYSDSHSLLSKCEPQAYP 366
 QY 106 ITEKGFVVPDLSHSHKPNFNL 127
 Db 367 PT---LHIPEITEKPNPEANI 385
 RESULT 15
 ID SERC_ARATH STANDARD; PRT; 430 AA.
 AC Q96255;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PHOSPHOSERINE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (EC 2.6.1.52)
 DE (PSAT).
 GN AT4G35630 OR F8D20.140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99097839; PubMed=9881164;
 RA Ho C.-L., Noji M., Saito M., Yamazaki M., Saito K.;
 RT "Molecular characterization of plastidic phosphoserine
 RT aminotransferase in serine biosynthesis from Arabidopsis.";
 RL Plant J. 16:443-452(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansoorge W., Brandt P., Griveill L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Billam L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenegger T., Bothé G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Clark L., Doggett J., Hall S., Cronin A., Quail M., Bray-Allen S.,
 RA Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
 RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Feiler R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
 RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Dedhia N., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

Search completed: April 22, 2002, 10:44:44
Job time: 190 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 22, 2002, 10:41:04 ; Search time 24.96 Seconds
(without alignments)
796.997 Million cell updates/sec

Title: US-09-601-490-1
Perfect score: 715
Sequence: 1 SSSFDKGYKGGDASYFEP.....SEHIKNPGFNLTWKVIEKK 136

Scoring table: BLOSSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	100.0	163	2 Q99SU7	Q99su7 staphylococ
2	710	99.3	163	2 Q9LC46	Q9lc46 staphylococ
3	703	98.3	163	2 Q9AM04	Q9am04 staphylococ
4	699	97.8	136	2 Q39Z29	Q39z29 staphylococ
5	138.5	19.4	416	2 Q9ZFE2	Q9zfe2 streptococ
6	88	12.3	569	10 Q9ZRR6	Q9zrr6 zea mays (m
7	87	12.2	348	2 Q34353	Q34353 bacillus su
8	84.5	11.8	483	9 Q9G004	Q9g004 bacterioph
9	83.5	11.7	606	2 Q9CMA9	Q9cma9 pasteurella
10	83	11.6	611	2 Q9X0Y4	Q9x0y4 thermotoga
11	82.5	11.5	16215	5 Q9NFS3	Q9nfs3 drosophila
12	81	11.3	526	2 Q9RQS7	Q9rqs7 mycoplasma
13	80.5	11.3	158	1 O59474	O59474 pyrococcus
14	78	10.9	350	10 Q39980	Q39980 hyoscyamus
15	77.5	10.8	1386	10 Q9LPB1	Q9lpb1 arabisdopsis
16	77	10.8	559	10 O65323	O65323 capsicum an
17	77	10.8	559	10 O81923	O81923 capsicum an
18	77	10.8	608	11 Q99JZ1	Q99jz1 mus musculu
19	76.5	10.7	289	1 O29463	O29463 archaeoglob

20	76	10.6	252	2 Q9CFA0	Q9cfa0 lactococcus
21	74.5	10.4	666	2 P96018	P96018 staphylococ
22	74	10.3	233	1 O29007	O29007 archaeoglob
23	74	10.3	233	5 Q9XUQ2	Q9xuq2 caenorhabdi
24	74	10.3	256	5 Q9XUQ3	Q9xuq3 caenorhabdi
25	74	10.3	428	12 Q9J501	Q9j501 fowlpox vir
26	74	10.3	462	10 O04622	O04622 arabisdopsi
27	74	10.3	480	10 Q9M156	Q9m156 arabisdopsi
28	74	10.3	552	2 Q9PPW0	Q9ppw0 ureaplasma
29	73.5	10.3	431	10 Q9XIR2	Q9xir2 arabisdopsi
30	73.5	10.3	764	3 O42976	O42976 schizosacch
31	73.5	10.3	1536	2 Q9X079	Q9x079 thermotoga
32	73	10.2	171	11 Q9CUN9	Q9cun9 mus musculu
33	73	10.2	345	13 Q9I946	Q9i946 gallus gall
34	73	10.2	470	10 O22732	O22732 arabisdopsi
35	73	10.2	654	10 Q9FRF0	Q9frf0 oryza sativ
36	73	10.2	875	4 Q9H706	Q9h706 homo sapien
37	73	10.2	2505	11 O63577	O63577 rattus norv
38	73	10.2	2509	4 Q16702	Q16702 homo sapien
39	73	10.2	2748	5 Q9V4P4	Q9v4p4 drosophila
40	73	10.2	4968	6 O29621	O29621 oryctoagrus
41	72.5	10.1	237	10 Q9XG34	Q9xg34 guillardia
42	72.5	10.1	584	2 O67429	O67429 aquifex aeo
43	72.5	10.1	666	2 O54272	O54272 staphylococ
44	72.5	10.1	666	2 O54277	O54277 staphylococ
45	72.5	10.1	2210	5 Q9GQV2	Q9gqv2 drosophila

ALIGNMENTS

RESULT 1

Q99SU7 ID Q99SU7 PRELIMINARY: PRT; 163 AA.

AC Q99SU7; DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE STAPHYLOKINASE PRECURSOR.

GN SAK OR SAI158.

OS Staphylococcus aureus subsp. aureus N315.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Staphylococcus.

OX NCBI_TaxID=158879;

RN [1]

RP SEQUENCE FROM N.A.

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino T., Kanamori M., RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K., RA Hirakawa H., Kuhara S., Goto S., Iabuzaki J., Kanehisa M., RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., RA Ogasawara N., Hayashi H., Furumatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";

RL Lancet. 357:1225-1240(2001).

DR EMBL; AF003135; BAB43032.1; -.

KW Complete proteome.

SQ SEQUENCE 163 AA; 18520 MW; 413CDAE14BE9FD40 CRC64;

Query Match 100.0%; Score 715; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 2.2e-54;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SSSFDKGYKGGDASYFEP	TPGLMVNVTGVDKGNELLS	SPHYVEPIKPGTTLTKKI	60
Db	28	SSSFDKGYKGGDASYFEP	TPGLMVNVTGVDKGNELLS	SPHYVEPIKPGTTLTKKI	87
QY	61	EYVWEALDATALYKEFRVWEL	PSAKIEVTYYDKNKKKEETK	SPITTEKGFVVPDLSEHI	120
Db	88	EYVWEALDATALYKEFRVWEL	PSAKIEVTYYDKNKKKEETK	SPITTEKGFVVPDLSEHI	147

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QY 121 KNPGENLITKVVIEKK 136
Db 148 KNPGENLITKVVIEKK 163

RESULT 2
Q9LC46 PRELIMINARY; PRT; 163 AA.
AC Q9LC46;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE STAPHYLOKINASE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219005; PubMed=10754251;
RA Horii T., Yokoyama K., Barua S., Odagiri T., Futamura N., Hasegawa T.,
RA Ohta M.;
RT "The staphylokinase gene is located in the structural gene encoding N-
RT acetylmuramyl-L-alanine amidase in methicillin-resistant
RT Staphylococcus aureus.";
RL FEMS Microbiol. Lett. 185:221-224 (2000).
DR EMBL; AB033232; BAA95011.1; -.
KW Kinase
SQ SEQUENCE 163 AA; 18474 MW; 3DB45E35046029DD CRC64;

Query Match 99.3%; Score 710; DB 2; Length 163;
Best Local Similarity 98.5%; Pred. No. 6e-54;
Matches 134; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSFDKGYKGGDASYFEPTGPLYLMVNTGVDKGNELLSPHYVEFPKPGTTLTKKI 60
Db 28 SSSFDKGYKGGDASYFEPTGPLYLMVNTGVDKGNELLSPHYVEFPKPGTTLTKKI 87

QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSPITEKGFVVPDLSEHI 120
Db 88 EYVVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSPITEKGFVVPDLSEHI 147

RESULT 3
Q9AM04 PRELIMINARY; PRT; 163 AA.
AC Q9AM04;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE STAPHYLOKINASE SAKXH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei W., Xiang H., Tan H.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332619; AAK11636.1; -.
KW Kinase
SQ SEQUENCE 163 AA; 18509 MW; 0A266B5EEAF65B5A CRC64;

Query Match 98.3%; Score 703; DB 2; Length 163;
Best Local Similarity 98.5%; Pred. No. 2.4e-53;
Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 121 KNPGENLITKVVIEKK 136
Db 148 KNPGENLITKVVIEKK 163

RESULT 4
Q93929 PRELIMINARY; PRT; 136 AA.
AC Q93929;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE STAPHYLOKINASE (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29213;
RA Chun H.S., Suk K., Kim S.H.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77328; AAB84174.1; -.
DR HSSP; P00802; ISSN.
FT NON_TER 1
SQ SEQUENCE 136 AA; 15551 MW; 79916BB136CA1A3F CRC64;

Query Match 97.8%; Score 699; DB 2; Length 136;
Best Local Similarity 97.8%; Pred. No. 4.3e-53;
Matches 133; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSFDKGYKGGDASYFEPTGPLYLMVNTGVDKGNELLSPHYVEFPKPGTTLTKKI 60
Db 1 SSSFDKGYKGGDASYFEPTGPLYLMVNTGVDKGNELLSPHYVEFPKPGTTLTKKI 60

QY 61 EYVVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSPITEKGFVVPDLSEHI 120
Db 61 EYVVEWALDATAYKEFRVVELDPSAKIEVYYDKNKKKEETKSPITEKGFVVPDLSEHI 147

RESULT 5
Q9ZFE2 PRELIMINARY; PRT; 416 AA.
AC Q9ZFE2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE STREPTOKINASE PRECURSOR (FRAGMENT).
GN SKC.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=87-542-W;
RA Caballero A.R., Lottenberg R., Johnston K.H.;
RT "Cloning, Expression, Sequence Analysis and Characterization of
RT Streptokinases Secreted by Porcine and Equine Isolates of
RT Streptococcus equisimilis.";

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RESULT 8
Q9G004 ID Q9G004 PRELIMINARY; PRT; 483 AA.
AC Q9G004;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF41.
OS bacteriophage phi ETA.
OC Viruses.
OX NCBI_TaxID=106284;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11115106;
RA Yamaguchi T., Hayashi T., Takami H., Nakasone K., Ohmishi M.,
RA Nakayama K., Yamada S., Komatsuzawa H., Sugai M.;
RT "Phage conversion of exfoliative toxin A production in Staphylococcus
RT aureus."
RL Mol. Microbiol. 38:694-705(2000).
DR EMBL; AP001553; BAA97627.1;
SQ SEQUENCE 483 AA; 55712 MW; DDBB2547E0DCEC80 CRC64;

Query Match 11.8%; Score 84.5; DB 9; Length 483;
Best Local Similarity 25.5%; Pred. No. 19;
Matches 27; Conservative 21; Mismatches 27; Indels 31; Gaps 5;

QY 29 VTGVDSKGNELSPHYVE-----FPIKPG-----TTLTKKIEYVVEWALDATAFYKEF 76
DB 139 LTGASNGKLEWHPYLDDEGEFKLRVPAEQIGPIWTDKHELEAFI----- 186

QY 77 RVVELDPSAKIEVTVYDKNKKKEKSPITEKGFVVPDLSEHIKN 122
DB 187 RMYKLENETKVE--IWDK-----VTVNYYVYENGSLIPDYSNNLEN 225

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RESULT 9
Q9CMA9 ID Q9CMA9 PRELIMINARY; PRT; 606 AA.
AC Q9CMA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FADD.
GN FADD_2 OR PM0925.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PM70;
RC MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006132; AAK03009.1;
DR InterPro; IPR000873; AMP-bind.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Complete proteome.
SQ SEQUENCE 606 AA; 69594 MW; FB500E49401E5224 CRC64;

Query Match 11.7%; Score 83.5; DB 2; Length 606;
Best Local Similarity 23.3%; Pred. No. 31;
Matches 38; Conservative 28; Mismatches 62; Indels 35; Gaps 8;

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QY 1 SSFDRKGYKKGDDASYFEPTGP-YLMVNVTVGVDSKGN-ELLSPHYVEPIKPGTTLTKR 58
DB 434 ADSFTEDGFLKTGDAGFDPOGNLYITDRIKELMTKNSGYIAPQYIE-----TKVGKD 487

QY 59 KIEYVVEWALDATAFYKEFRVV-----ELDPSAK-IEVTVYDK-----NK 96
DB 488 KFIEQIAVIADAKYVVSALIVPCFNSLEAYAKQLNIKHDRLELIKHSIDILQMFEQRIND 547

QY 97 KKEETKSPITEKGFVVPDL-----SEHIKNPGFNLTIVKVIK 135
DB 548 LQKELPSFEQIKKFTLLPQAFTTKMEEI-TPTLKLRKRVILER 589

RESULT 10
Q9X0Y4 ID Q9X0Y4 PRELIMINARY; PRT; 611 AA.
AC Q9X0Y4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN TM1257.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
DR EMBL; AE001781; AAB36331.1;
DR TIGR; TM1257;
KW Complete proteome.
SQ SEQUENCE 611 AA; 70010 MW; 7FB042D4E49097AB CRC64;

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Query Match 11.6%; Score 83; DB 2; Length 611;
Best Local Similarity 21.5%; Pred. No. 34;
Matches 28; Conservative 27; Mismatches 45; Indels 30; Gaps 5;

QY 8 KYKKGDDASYFEPTG-----PYLMVNVTVGVDSKGN-----ELLSPHYVEEPIKP 51
DB 163 RYILCDNGAHINVSQSGVAAKTSYTFVLVKSMIETSKNDGDLMLREURARYIIFNVKG 222

QY 52 GTTLTKKIEYVVEWALDATAFYKE-FRVVELDPSAKIEVTVYDKNKKKEETKSPITEKG 110
DB 223 ESSLFLDRIS--KEMYSEREKWDENVRLGIEPKPEENVAFY-----APSRKRG 269

QY 111 FVVPDLSEHI 120
DB 270 AYIPDVNKRLL 279

RESULT 11
Q9NFS3 ID Q9NFS3 PRELIMINARY; PRT; 16215 AA.
AC Q9NFS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE D-TITIN.
GN SLR OR D-TITIN OR CG1915.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

```

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.Q., Broadie K.S.;
RT "Characterization of Drosophila D-Titin gene";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AJ271740; CAB93524.1; -;
DR FlyBase: FBgn0003432; sIs.
DR InterPro: IPR002106; AA_TRNA_ligase_II.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00041; fn3; 5.
DR Pfam: PF00047; Ig; 48.
DR Pfam: PF00018; SH3; 1.
DR SMART: SM00408; IGC2; 15.
DR SMART: SM00410; IG_Like; 34.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
DR PROSITE: PS0002; SH3; 1.
SQ SEQUENCE 16215 AA; 1841509 MW; 242C8765E00F7603 CRC64;

Query Match 11.5%; Score 82.5; DB 5; Length 16215;
Best Local Similarity 25.5%; Pred. No. 2.1e+03;
Matches 36; Conservative 32; Mismatches 52; Indels 21; Gaps 8;

QY 8 KYKGGDASVFE-----PTGPLYMVNV-TGVDSKG-NELLSPHYVEPIKPGTTLTK 57
Db 10444 RHEKGEVQVLVESVAPGEPFVEINVISSANTEGDSEITTDKIK---KKSRIKK 10500

QY 58 EKEYYVEWALDATAKEFRVVELDSAKTEVYYDKNKKETKS-FPITEKGFVVP-D 115
Db 10501 DDLDAVYIQQLNA-----EIPVTELEYEKIDVDGKAKPKKAKTKKPIIDEGETLQVG 10556

QY 116 LSEHKPNPGFNLTQVVKIEK 136
Db 10557 VTEH--EPTKKLTKKPEEK 10575

RESULT 12
Q9RS7
ID Q9RS7 PRELIMINARY; PRT; 526 AA.
AC Q9RS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MAJOR LIPOPROTEIN PRECURSOR.
GN LPPA.
OS Mycoplasma mycoides subsp. mycoides LC.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Entomoplasmataceae.
OX NCBI_TaxID=44100;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y-GOAT;
RX MEDLINE=99167669; PubMed=10066658;
RA Monnerat M.P., Thiaucourt F., Poveda J.B., Nicolet J., Frey J.;
RT "Genetic and serological analysis of lipoprotein LppA in Mycoplasma
RT mycoides subsp. mycoides LC and Mycoplasma mycoides subsp. capri.";
RL Clin. Diagn. Lab. Immunol. 6:224-230(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y-GOAT;
RX MEDLINE=99440592; PubMed=10512041;
RA Monnerat M.P., Thiaucourt F., Nicolet J., Frey J.;
RT "Comparative analysis of the lppA locus in Mycoplasma capricolum

RT subsp. capricolum and Mycoplasma capricolum subsp. capripneumoniae.";
RL Vet. Microbiol. 69:157-172(1999).
DR EMBL: AF072714; AAF06069.1; -;
KW Lipoprotein.
SQ SEQUENCE 526 AA; 60287 MW; 605CED85B652249D CRC64;

Query Match 11.3%; Score 81; DB 2; Length 526;
Best Local Similarity 23.7%; Pred. No. 42;
Matches 41; Conservative 24; Mismatches 64; Indels 44; Gaps 6;

QY 2 SSFDKGYKKGD-----DAS-----YFEPTGPYL-----MVNVGT 31
Db 218 TEIDKNNKKYDIKPKETVDSRLSGLYPSILAYMLYAEYNNYKSLQETDKDAINFEG 277

QY 32 VDSKGNELLSPHYVEPIKPGTTLTKIEKYVEWALDATAKYK----EFRVVELDPSAKI 87
Db 278 LINKPTNLFNDFKVFVSGV-----TKELLDFENYRKLYVKLVGAGFDDINGTLTKV 332

QY 88 EYVYDKNKKKEETKSPITEKGFVVPDLSEHKPNPGFNLT-----KVVIETK 135
Db 333 EINNSEENKEKEPGISKEFSFKGFRKVTNDEPSKNPFVSLTPADLKKIITDK 385

RESULT 13
O59474
ID O59474 PRELIMINARY; PRT; 158 AA.
AC O59474;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 18.1 KDA PROTEIN PH1810.
GN PH1810.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000007; BAA30929.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 158 AA; 18113 MW; 761428F02518AF06 CRC64;

Query Match 11.3%; Score 80.5; DB 1; Length 158;
Best Local Similarity 27.0%; Pred. No. 11;
Matches 33; Conservative 16; Mismatches 38; Indels 35; Gaps 5;

QY 38 ELLSPHYVEPIKPGTTLTKEK-----IEYYVEWALDATAKYKFRVVELDPS 84
Db 4 DILKPEYIAFTIKEREKLEKKAQTIETPGSEYEIATVEYFVDSIFERFIYIARSDS 63

QY 85 AKTEVYYDKNKKKEETKSPITEKGFVVPD-----LSEHKN-----PGNLTIKV 131
Db 64 ILVA-----RSSEKINTKG-----EKKELVKDKGLKRLILLSEISKSKVKVGTGKINFILAT 114

QY 132 VI 133
Db 115 II 116

RESULT 14
Q39980

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ID Q39980 PRELIMINARY; PRT; 350 AA.
AC Q39980;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE VETISPIRADIENE SYNTHASE (FRAGMENT).
OS HYOSCYNAMUS MUTICUS (EGYPTIAN HEMBANE).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Hyoscyamus.
OX NCBI_TaxID=35626;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95221394; PubMed=7706281;
RA Back K., Chappell J.;
RT "Cloning and bacterial expression of a sesquiterpene cyclase from
RT Hyoscyamus muticus and its molecular comparison to related terpene
RT cyclases."
RL J. Biol. Chem. 270:7375-7381(1995).
DR EMBL; U20190; AAA86339.1; -.
DR HSP; Q40577; SEAU.
DR Mendel; 11835; Hyomu;2509;11835.
DR InterPro; IPR001906; Terp_synth_fam.
DR Pfam; PF01397; Terpene_synth; 1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 41104 MW; FEE71BC7BEADAAE CRC64;

Query Match 10.9%; Score 78; DB 10; Length 350;
Best Local Similarity 32.8%; Pred. No. 46;
Matches 22; Conservative 14; Mismatches 23; Indels 8; Gaps 4;

QY 59 KIEYVEWALDATAYKEFRVVELDSAKTEVYYDKNKKKEETKSFPTTEKGFV---VPD 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 KISKYK--LLD--LYKDYB--TELSKDGSRVVHYAKRMKEIVRYFVEAKWFIEGYMPP 192
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QY 116 LSEHIKN 122
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Db 193 VSEYLN 199

RESULT 15
Q9LPB1 PRELIMINARY; PRT; 1586 AA.
ID Q9LPB1
AC Q9LPB1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE T32E20.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen B., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T32E20 from chromosome
RT I."
RN Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;

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RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[4]

RN SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen B., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE
CC TRANSCRIPTASE).
DR EMBL; AC020646; AAF79809.1; -.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1586 AA; 180875 MW; A9D3917EAFDAD790 CRC64;

Query Match 10.8%; Score 77.5; DB 10; Length 1586;
Best Local Similarity 30.4%; Pred. No. 33e+02;
Matches 31; Conservative 14; Mismatches 36; Indels 21; Gaps 5;

QY 34 SKGNELLSPHVVEPPKPGTT-----LTKEKIEYVEWAL-----DATAKKEFR 77
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1412 AKLMDTLWAYRTAFKTPDGTTPFNLLYGRKSHLPVE--LEYKAMWAVKLLNFDIKTAEKR 1470
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 78 VVELDPSAKIEVTVYDKNK--KKEETKSF---PITEKGFVVPD 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1471 LIQLNDLKNIRLEAYESSKIKYKERTKSFHDKKIVSRDFKVG 1512
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Job time: 203 sec

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